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Score
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1: /cgn2_6/ptodata/2,
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3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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US-08-466-151-2
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Sequence 16, Appl	Sequence 2, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 18, Appl	Sequence 17, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 4, Appli	Sequence 26, Appl		Sequence 26, Appl	Sequence 33, Appl		Sequence 73, Appl	Sequence 73, Appl

ALIGNMENTS

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RESULT 1
US-08-483-636-2
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                                                                            TELEFAX: (215) 270-509
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                        NAME: Sutton, Jeffrey A.
REGIZENT NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P5'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Holmes, Stephen D. APPLICANT: Gross, Mitchell S. APPLICANT: Sylvester, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
  MOLECULE TYPE:
                                       LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Box 1539
CITY: King of Prussia
STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                       TOPOLOGY:
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                                       amino acid
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O. Box 1539 / UW2220
protein
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Sequence

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US-08-483-632-2
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Best Local Similarity
                                                       Matches
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Patent No. 5928904
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Best Local S
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APPLICANT: Holmes, Stephen D.

APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant II4 Antibodies Useful in TITLE OF INVENTION: Treatment of II4 Mediated Disorders NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US/94/10308 FILING DATE: 07-SEP-1994 ATTORNEY/AGENT INFORMATION:
NAME: SULLON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                           TELEFAX: (215) 270-50 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 1
FILING DATE: 14-OCT-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.U. CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
                                                                                                                                                                               LENGTH:
                                                      104;
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P.O. Box 1539 / UW2220
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                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER: US 08/136783
14-OCT-1993
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93.7%;
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93.78;
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RESULT·4
US-08-579-378A-14
; Sequence 14, Application
; Patent No. 6210671
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Best Local Sim
Matches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHIOSAKI, Kouich
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: TOKIYOSHI, Sachi
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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TYPE: a
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ZIP: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Browdy, Roger L. REGISTRATION NUMBER: 2
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                                                                                                                60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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                                                                                                                                                                                                                                             Similarity
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                                                                                                GIPARFSGSGSGTDFTLNIHPVEEEDGATYYCQQSNEDPWTFGGGTKLETK 111
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EDA, Yasuyuki
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Pred. No. 1.4e-47;
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                                                                                                                                                    Sequence 6, Application US/08466151 Patent No. 6037453
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APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 14:
                                                              APPLICANT: Jardieu, Paula M. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Immunoglo NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9:
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew
STREET: One Marketplaza, Steuart Tower, Suite 2000
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                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 90.1 nes 100; Conservative
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CITY: San Francisco
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                 STREET:
                                ADDRESSEE:
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South San Francisco
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                E: Genentech, Inc.
1 DNA Way
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90.1%;
                                                                                Immunoglobulin Variants
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Pred. No. 3.5e-47;
4; Mismatches 6;
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718p2c1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
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APPLICATION NUMBER: 07/879495

FILING DATE: 07-MAX-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744768

FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: US 07/744,768 PRIOR FILING DATE: 1991-08-14
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/405617
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Amino Acid
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   Query Match
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                                                                                                            INFORMATION FOR SEQ ID NO: 2:
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               )8-466-151-2
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acid
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No. 6037453
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-7011-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/11 FILING DATE: 26-JAN-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                          TELEPHONE: 650/225-1489
                                                                                                                                                                                                                    FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Immunoglobulin Variants NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jardieu,
APPLICANT: Presta, I
                                                                                                                             TELEFAX:
                                                                                                                                                                         NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2ClD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                               TOPOLOGY:
                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/744768 FILING DATE: 14-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGT 105
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                                                                             111 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
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93.4%;
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   84.5%;
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Pred. No. 6.4e-46;
 Score
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   491.5;
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Length 111;
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                                                                                                                                                                                                                                                                            Sequence 24, Application Patent No. 5558865
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Patent No. 6329509
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Best Local
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PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1991-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1995-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/466,163B CURRENT FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Immunoglobulin Variants FILE REFERENCE: p0718P2ClD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 111
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  STREET: Chicago
CITY: Chicago
TMATE: Illinois
HSA
                                                                                                                                                                                                                             APPLICANT: Ohno, T
                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
           SOFTWARE:
                                                                                                                                                                   ADDRESSEE:
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APPLICATION DATA:
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                                                                                                                                                   6300 Sears Tower, 233 S. Wacker Drive
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            PatentIn Release #1.0,
                                                                                                                                                                                  Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                         Tsuneya
N: HIV Immunotherapeutics
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Pred. No. 1.2e-44;
3; Mismatches 9;
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3; Mismatches 9;
              Version
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                #1.25
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CLASSIFICATION:

APPLICATION NUMBER: FILING DATE:

08/111,080

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RESULT 10
US-08-211-980-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-630
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Ohno, '
                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/U
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 310
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                     STREET: 6300 Street: Chicago STATE: Illinoi:
APPLICATION NUMBER: US 08/039,457 FILING DATE: 22-APR-1993
                                                                                                   CLASSIFICATION:
                                                                                                                      FILING DATE:
                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                   Illinois
                                                                                                                                                                                                                                                                                                                    6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                     USA
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/ENTION: HIV Immunotherapeutics
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                                                                                                                                 US/08/211,980
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Pred. No. 1.7e-44;
3; Mismatches 10
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TOPOLOGY: li;

MOLECULE TYPE:
PCT-US93-07967-24
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Chicago
CITY: Chicago
TMATE: Illinois
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ohno, Tsuneya
                                                                                                                                                                                                               FILING DATE: 22-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                           TELLEFAX: (**. 25-3856
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                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                        LENGTH:
                                                                                                                                                                                                NAME: Borun, Michael F
                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                        (312) 474-0448
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                              linear
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Pred. No. 1.7e-44;
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RESULT 13
US-09-109-207C-5
; Sequence 5 Application US/09109207C
; Patent NO. 6172213
; GENERAL INFORMATION:
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Best Local S
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Best Local :
    APPLICANT:
TITLE OF IN
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODONA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/25-9881
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/887,352B FILING DATE: 03-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
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                                                                                                                                                            60 GIPARFSGSGGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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    INVENTION:
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                                                                                                                                                                                                                                                                                                                                                    Linear
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                 Lowman,
 Improved
                                                                                                                                                                                                                                                                                      83.48;
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87.3%;
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 Leonard G. Presta, Pa
d Anti-IgE Antibodies
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Pred. No. 5.3e-44;
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Pred. No. 1.7e-44;
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 Presta, Paula
Antibodies and
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M. Jardieu, John Lowe
Method of Improving Polypeptide
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; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-109-207C-5
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US-08-483-636-58
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US-09-296-005-5
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                                                                                                                                                                                        Sequence 58, Application US/08483636 Patent No. 5914110
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LENGTH: 111
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Best Local :
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                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Holmes
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 STREET:
                              ADDRESSEE:
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97; Conserv
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                Intellectual Property
D. Box 1539 / UW2220
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Pr
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P1123C1r
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EARLIER FILING DATE: 1997-07-02
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/296,005 FILING DATE: 1999-04-21
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Pred. No. 5.3e-44;
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Pred. No. 5.3e-44;
3; Mismatches 10
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es and Method of Improving Polypepti
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CURRENT APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/117366
FILING DATE:
CLASSIFICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA: US 08/136783
PRIOR APPLICATION NUMBER: US 08/136783
PRIOR APPLICATION NUMBER: PCT/US/94/10308
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REFIGISTRATION NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEPHONE: (215) 270-5024
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TOPOLOGY: 1inear
MOLECULE TYPE: protein
US-08-483-636-58
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Best Local S
Matches 89
Arch completed: September 13, 2003, 07:56:02 ob time : 30 secs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                 tch 80.7%; Score 469.5; DB 2; Length 131; al Similarity 80.2%; Pred. No. 3.1e-42; 89; Conservative 8; Mismatches 13; Indels 1
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                                           and is
                                                                                                                                                                                                                    Pred. No.
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537.5
537.5
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                                                                                                                                                                                         No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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length: 2000000000
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582
1 DIVLTNSPASLAVSL
                                                                                                                              Match
                                                                                                                                           Query
                                                                                                                                                                                                                                                                                      1107863 seqs, 158726573 residues
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003
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AAR70189
AAY23767
AAY18120
AAY59267
AAY51144
AAY51146
AAY59264
                                                                                                                                                                  SUMMARIES
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235.945 Million cell updates/sec
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Mouse MAb 3B9 ligh
Light chain variab
Light chain sequen
Antibody 4H5 L cha
Murine derived pro
Murine derived pro
Antibody 4H5 H cha
Antibody 4H5 L cha
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111 238	111	238	238	238	238	238	218	218	120	111	111	103	103	112	106	106	131	222	113	131	111	111	131	111	111	238	238	238	238	238	238	238	305	305
19	20	23	23	21	21	19	24	24	15	21	14	21	21	22	21	14	11	18	22	10	23	10	14	15	15	24	23	23	23	21	21	19	21	21
AAB76939 AAW83032	565	493	68	AAW90924	AAB14774	303	ABP96774	677	GD.	AAY85193	AAR33305	AAY51140	AAY59263	AAB62872	AAY85197	AAR33309	AAR04132	AAW01751	AAB71895	AAP90543	AAU99852	AAP90541	AAR32123	AAR60302	UЛ	ABG76346	1837	7491	486	89	474	0	114	AAY51141
Variable light cha Anti-Fas humanised	musculus ar	ant		anti-	Humanised anti-Fas	i-Fas huma		ptor	uence of t		MaEll light chain.	æ	Antibody 4H5 L cha		Light chain amino	light	Leu 3a	MH1 monoclonal ant	Monoclonal antibod	S	Mouse AC10 antibod	Ā	CD4	Anti HIV antibody	e anti-H	Mouse DAV-1 light	¢		Humanised anti-Fas	ne anti-Fas	se anti-Fas	Ŧ	derived p	Murine derived pro

ALIGNMENTS

RESULT 1 AAO18536 11-JAN-2002; 2002WO-US00927. Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection. 11-OCT-2002 (first entry) AA018536 standard; Protein; 11-JAN-2001; 2001US-0759112 18-JUL-2002. WO200255668-A2 Mus sp. Murine Mab 1F7 light chain. (IMMP-) IMMPHERON INC 110 8

New polynucleotide encoding a complementarity or framework-determining

N-PSDB; AAL48661 WPI; 2002-590668/63.

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RESULT 2
AAR70189
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Best Local S
Matches 110
                                          Gross
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in vaccines against HIV \, -
         N-PSDB;
                                                                                                07-SEP-1993;
14-OCT-1993;
                                                                                                                                 07-SEP-1994;
                                                                                                                                                       16-MAR-1995
                                                                                                                                                                                                                                                       Region
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20-SEP-1995
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                    WPI; 1995-123387/16
                                                                                                                                                                            W09507301-A1
                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                    Mouse
                                                              (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                             Peptide
                                          MS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Page 23-24; 27pp; English.
          AAQ83490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG
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                                          Holmes
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(first entry)
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                                                                                              93US-0117366.
93US-0136783.
                                                                                                                                 94WO-US10308
                                                                                                                                                                                                                        /note= "complementarity
113..121
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                                                                                                                                                                                                                                                                                        /label= Sig_peptide
                                                                                                                                                                                                           /label-
                                                                                                                                                                                                                                            /label= CDR
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                             /label- CDR
                                         SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                                                 "complementarity
                                         Sylvester
                                                               CORP.
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                                         DR
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RESULT 3
AAY23767
ID AAY2
XX AAY2
XX AAY2
AC AAY2
XX Ligh
KW Chin
KW Chin
KW Conj
KW Conj
KW Conj
XX US5:
XX US5:
XX O7-,
PR 07-,
PR 07-,
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PR 07-,
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                                                                                                                                                                                                                                                                                                                      07-SEP-1993;
14-OCT-1993;
07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease;
                                                                                                                                                                                                              Gross MS,
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                                         Example 3;
                                                                                 treating
                                                                                                     New DNA molecules encoding
                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                        (SMIK
                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
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DB; AAX85884.
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                                                                                 IL4-mediated
                                       Fig
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93US-0117366.
93US-0136783.
94WO-US10308.
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K
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humanised
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                                                                                     conditions
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                                         English
                                                                                                                                                                                                                                                        CORP
                                                                                                       recombinant antibodies
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Pred.
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antibody; IL-4
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No. 1e-38;
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mediated allergic
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                                                                                                       useful
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RESULT 4
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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                    07-SEP-1993;
14-OCT-1993;
07-SEP-1994;
This sequence represents the light chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IIA) monoclonal antibody for the treatment immunoglobulin E (IgE) mediated diseases. The antibodies are useful the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shall represent the antibodies are also useful for regulating B and T cell prolifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; interleukin-4; II.4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. b ELISA of circulating endogenous IL-4 levels in humans.
                                                                                                                         Claim
                                                                                                                                                                                                                             Gross
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                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
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                                                                                                                                                     Recombinant IL4 antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain sequence
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DB; AAX79519.
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                                                                                                                      24; Fig 1; 50pp; English.
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93US-0117366.
93US-0136783.
94WO-US10308.
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BEECHAM PLC.
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93.7%;
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Best Local :
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                                                                                                                        The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 445 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents a L chain fragment of the antibody 445.
                                                                                                                                                                                                                                                                                                                       Mus
                                                                                                         Sequence
                                                                                                                                                                     Disclosure;
                                                                                                                                                                                     An antibody and the nucleic acid coding
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                                                                                                                                                                                                                                                                                                                                       CD4 antigen;
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DB; AAZ58690.
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                                  DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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                  GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                        anti-human; antibody; 4H5;
                                                                                                                                                                                                                                                                                                                                                          L chain
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                                                                      Score 532.5; DB :
Pred. No. 2.3e-38;
2; Mismatches !
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RESULT 6 AAY51144

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoletic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HTV infection and autoimune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
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        Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation, HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 95; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devices containing antibodies recognising CD4 or CD34 and their use the separation of CD4 or CD34 positive cells \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-086720/07
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                                                                 Murine derived protein fragment #8.
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26-MAY-1998;
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                                                                                                                                                    AAY51146 standard;
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103; Conserv
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ASAHI MEDICAL CO LTD
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                                                                                                                                                                                                                        GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSSEDPPTFGGGTKLEIK 111
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98JP-0163023.
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                                                                                                                                                    Protein; 111 AA.
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92.8%;
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Pred. No. 2.3
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26-MAY-1998;
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                                                                                         JP11332563-A
                                                                                                                                     CD4 antigen;
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                      26-MAY-1998;
                                            26-MAY-1998;
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                                                                                                                                     anti-human; antibody;
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 KASEI KOGYO KK
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98JP-0163023.
                      98JP-0163034.
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AAY59265
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                                        Query Match
Best Local S
Matches 103
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Best Local S
Matches 103
                                                                                                 The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 445 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain sequence of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 445 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain sequence of the antibody 4H5.
                                                                                 Sequence
                                                                                                                                                  Disclosure; Page 17-18; 25pp; Japanese.
                                                                                                                                                                                            N-PSDB; AAZ58664
                                                                                                                                                                                                                                                                26-MAY-1998;
                                                                                                                                                                                                                                                                                                        JP11332563-A
                                                                                                                                                                                                                                                                                                                           Mus sp
                                                                                                                                                                                                                                                                                                                                               CD4 antigen;
                                                                                                                                                                                                                                                                                                                                                                 Antibody 4H5
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY59265 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                      An antibody and the nucleic acid coding the antibody
                                                                                                                                                                                                                        (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                            26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                     17-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                         AAY59265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 16-17; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An antibody and the nucleic acid coding the antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                     2000-091351/08.
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)B; AAZ58663.
   156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                  Similarity
DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                 305
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                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                               anti-human;
                                                                                                                                                                                                                                                                                                                                                                 L chain sequence
                                                                                                                                                                                                                                                                                                                                                                                     (first
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                                                                                                                                                                                                                                            98JP-0163034
                                                                                                                                                                                                                                                                98JP-0163034
                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.5%;
                                                 91.5%;
                                                                                                                                                                                                                                                                                                                                              antibody;
                                       Pred. No. 6.3e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e 532.5; Ub ...
                                                                                                                                                                                                                                                                                                                                              4H5; drug.
                                   ; DB 21,
6.3e-38;
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                        Indels
                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                        ۲.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
  215
                    59
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RESULT 10
AAY51141
ID AAY51
AC AAY51
XX AAY51
XX AAY51
XX AUTIN
XX AUTIN
XX AUTIN
XX Clust
KW Clust
KW HIV 1
XX Hemat
XX Hemat
XX Hemat
XX Hemat
XX 25-M
PR 26-M
XX 25-M
PR 26-M
XX AUTIN
PR AUTIN
PR WPI;
PR Clain
XX AUTIN
PR CC This
CC This
CC This
CC Comp

RESULT 11
AAY51142
ID AAY51
                                                                                                                                                                                                                                                                                                                                                              Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (Chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoletic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASAH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cluster differentiation; cell separ
hematopoietic; undifferentiated; ly
HIV infection; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Devices containing antibodies the separation of CD4 or CD34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-1998;
26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hematopoietic;
HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ono M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9961629-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-086720/07.
DB; AAZ44205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                 Soka T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASAHI KASEI KOGYO KK
ASAHI MEDICAL CO LTD
                                                                                                                                       GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSSEDPPTFGGGTKLEIK 133
                                                                                                                                                                                             GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 80-82; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 AA;
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0159957
98JP-0163023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                        91.5%;
92.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305
                                                                                                                                                                                                                                                                                                                                                              2:
                                                                                                                                                                                                                                                                                                                                                                                        Score 532.5; DB 2
Pred. No. 6.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            positive cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recognising CD4 or CD34 and their use for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      separation; antibody; CD4; CD34; leukemia;
ed; lymphocyte; bone marrow transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miyamura
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocyte;
e; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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AAY51142

standard;

Protein;

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RESULT 12
AAW83042
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                                                                                                                                                                                                                                                                                                est Local S
atches 103
                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HJV infection and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASAH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                          Anti-Fas MAb HFE7A light chain.
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-1998;
26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09961629-A1
                                                       25-MAR-2003
15-MAR-1999
                                                                                                                        AAW83042 standard; Protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Devices containing antibodies recognising CD4 or CD34 and their use the separation of CD4 or CD34 positive cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ44206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ono M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine derived protein fragment #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY51142;
                                                                                                                                                                                                                                                                                                                                                                              is sequence represents a murine derived protein fragment which is used illustrate the method of the invention.
                                                                                                                                                                                          216
                                                                                                                                                                                                                                             156
                                                                                                                                                                                                                                                                                                103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-086720/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Page 82-84; 111pp; Japanese.
                                                                                                                                                                                                                   60
monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                        1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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ASAHI
                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                        GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                            DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                     305
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDICAL CO LTD
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98JP-0163023.
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                                                                                                                                                                                                                                                                                                             91.5%;
92.8%;
                                                                                                                                                                                                                                                                                              Score 532.5; DB Z1;
Pred. No. 6.3e-38;
Pred. No. 6.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyamura
                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                                                                                                                                                           305;
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WARRAND WARRED FFFFFFFFFFFF WARRAND AND WARRAND WARRAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1997;
01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masahiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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O, Nobufusa
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97JP-0082953.
97JP-0169088.
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113..121
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132..238
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21..131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hiroko Y,
S, Shin Y
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(, Tohru
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myocarditis, diseases e.g. autoimmune disease, New antibodies and proteins bind New antibodies and proteins bind conserved epitope of Fas antigen seed to evaluate drugs in animal models and to treat Fas-associated hepatitis and allergy, atopy, arteriosclerosis,

WPI; 1998-543440/01. N-PSDB; AAV70130.

Reference Example 4; Page 189-190; 292pp; English.

chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828) RT-PCR (see ANV70127-28). The invention provides humanised HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These antibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic-lupus erythematosus, Hashimoto's disease, graft versus host disease, signers syndrome, pernicious anaemia, Addison's disease. arthritis, autoimmune haemolytic anaemia, sterility, myasthenia scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid monoclonal antibody HFE7A. This is the amino acid of the light chain of murine anti-human cDNA (see AAV70130) encoding the light thrombopenia purpura

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B14748
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Best Local
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                                                   (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, allergy, aplastic anaemia (panmyelophthis), hepatitis, AID; and organ graft rejection who present
                                                                                                                                                or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The antibody as the active component antibody is either the murine anti-human Fas monoclonal antibody or a humanised version of HFE7A containing identical CDRs
         and organ graft rejection. The present sequence represents the light chain of the murine anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).
                                                                                                                                                                                                                                                                              anti-Fas antibody
                                                                                                                                                                                                                                                                                         Preventive or treating in the Fas/Fas ligand s
                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1998;
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                                                                                                                                                                                                               The invention relates to compositions
                                                                                                                                                                                                                                              Example 4; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine; complementarity determining region; CDR; human Fas;
Fas ligand; apoptosis modulator; programmed cell death;
autolmmune disease; allergy; atopy; arteriosclerosis; myocarditis;
cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse anti-Fas antibody HFE7A light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 - NOV - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14748 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-Fas antibody; monoclonal antibody HFE7A;
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92.8%;
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                                                                                                                                                                                                                                                                                       for the diseases caused by e.g. autoimmune diseases, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 528.5;
Pred. No. 1.
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RESULT 14
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molecule (I) that, induces apoptosis in cells with an prevents ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosurpressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia, Addison's disease; scheroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple scherosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                                                                                                            This invention
                                                                                                                                                                                                                                                                                                                                                             Example reference 4; Page 104; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serizawa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SANY ) SANKYO CO LTD.
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30-SEP-1998;
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DB; AAA11547.
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anti-arthritic; antiviral; immunomodula
                                                                                                                                                                                                                                                                                                            describes a novel humanized anti-Fas antibody-like
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98JP-0276882
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RESULT 15
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             The invention relates to a preventive or treating agent for diseases caused by abnormality in FasyFas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP2001342148-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; allergy; atopic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
light chain subunit; apoptosis; immunosuppressive; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised anti-Fas antibody related peptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB74867 standard; Peptide; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                    Example 6 (Preparatory); Page 26; 194pp; Japanese.
                                                                                                                                                                                                                            treating autoimmune diseases, allergy, and atopy
                                                                                                                                                                                                                                                                                                                                                                29-MAR-2000; 2000JP-0090918
                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method of the invention.
                                                                                                                                                                                                                                                                                                                          (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                              containing humanised anti-Fas antibody, used for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
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is used
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Pred. No. 1.1e-37;
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                                                                                                                    September 13,
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                                                      KVMSM6
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Ig kappa chain V region (PC7043) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C;Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: A01937

RESULT KVMS43

В Ş

61 60

GIPARESGSGSTDFTLNIHPVEEEDAATYYCQLCNEDPPTEGAGTKLELK

110

A;Molecule type: protein
A;Residues: 1-111 <WEI>
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing
A;Reference number: S42176; MUID:94009207; PMID:7691608

B cells

with

A; Reference number: A; Accession: S42187 A; Molecule type:

Qy 1 DIVLTNSPASLAVS:	Query Match Best Local Similarity 94. Matches 105; Conservative	A;Accession: B0193/ A;Molecule type: protein A;Residues: 1-11 <wei> C;Complex: An immunoglobulin heterotetramer subunit consists of two id hain disulfide bonds. In some cases, such as IgA and IgM, the subunits C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:16-94/Domain: immunoglobulin homology <imm> F;23-92/Disulfide bonds: #status predicted</imm></wei>	R; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L. Nature 276, 785-790, 1978 A; Title: Rearrangement of genetic information may produce immunoglobulin diversity. A; Teference number: A93204; MUID:79073152; PMID:103003	RESULT 1 KVMS83 Ig kappa chain V region (PC7183) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change C;Accession: B01937; A01937		405.5 69.7 405.5 69.7 403.5 69.3	417 71. 415.5 71. 415.5 71. 415.7 71.	420.5 424.5 421.5 417.5		430.5 74.0
LGQR 	91.7%; 94.6%; tive	het e ca o V immu in h	; Lo neti MUID	183) se m		2221	งผผม	2212	2222	ㅂ
DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES	Score 533.5; DB 1; Pred. No. 2.6e-41; 0; Mismatches 5;	erotetramer subunit consistses, such as IgA and IgM, region; immunoglobulin homology <imm></imm>	Loh, E.; Schilling, J.; Hood, tic information may produce i JID:79073152; PMID:103003	(PC7183) - mouse (house mouse) uence_revision 30-Jun-1993 #text_cl 937	ALIGNMENTS	PH1077 PH1079 PH3079 S37202	PH0092 PH0093 E53285	KVMS32 S09965 PH1076		KVMS54
3QPP	Length 111; Indels 1	ts o the olog	immu	hang		Pi Pi Pi	ى د			
KLLTY KLLTY	111; 1;	f two subur y	noglo			light light light kappa	kappa kappa kappa	kappa kappa kappa light	kappa kappa kappa kappa	kappa
AASNLES 59 AASNLES 60	Gaps 1;) identical light (its associate into	bulin diversity.	21 - Jan - 2000		chair chair chair chair	cha cha cha	chain chain chain chain	chain chain chain chain	chain V

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A; Molecule type: protein
A; Residues: 1-111 <WEIV
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin.
                                                                                                                                                                                                   Ig kappa chain V region (PC6308) - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-20 C;Accession: CO1937; AO1937 R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L. Nature 276, 785-790, 1978 A;Title: Rearrangement of genetic information may produce immunoglobulin A;Reference number: A93204; MUID:79073152; PMID:103003 A;Accession: CO1937
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
F;13-92/Disulfide bonds: #status predicted
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A; Residues: 10-99 <MOO>
A; Cross-references: EMBL:225454; NID:g407842; PIDN:CAA80941.1; PID:g407843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z25452; NID:g407840; A;Note: V-kappa-21E; anti-collagen A;Accession: S42192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 15-99 < MOA>
A; Cross-references: EMBL: Z25448; NID: g407836;
A; Note: V-kappa-21E; anti-collagen
A; Accession: S42188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: V-kappa-21E; anti-collagen A; Accession: S42189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 12-99 <MOW>
A; Cross-references: EMBL: Z25458; NID: g407844;
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A;Cross-references: EMBL:225444; NID:g407832; PIDN:CAA80931.1; PID:g407833
A;Note: V-kappa-21E; anti-collagen
                          F; 23-92/Disulfide bonds:
                                             F;16-94/Domain:
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A; Residues: 10-99 <MOY>
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esidues: 12-99 <MOZ>
cross-references: EMBL:Z25446; NID:g407834;
Note: V-Kappa-21E; anti-collagen
A;Accession: S42191
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Matches 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                             immunoglobulin homology <IMM>
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                     #status predicted
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Pred. No. 8.9e-41;
2; Mismatches 5
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Gene 121, 271-278,
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                                                                   F;36-114/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: PH1226
Query Match
Best Local
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  Similarity
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g

89.6%; 90.1%;

Score Pred.

521.

3.6e-40;

Length 131;

gen

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Gene 121, 271-278, 1992
A;Title: Combinatorial functions of two chimeric antibodies
A:Reference number: PH1224; MUID:93077041; PMID:1446824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin C:Keywords: heterotetramer; immunoglobulin E:16-94/Domain: immunoglobulin homology <IMM>
                                                                           A;Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766 A;Note: this mouse sequence was hybridized and fused with a human consta C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                         Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; A;Experimental source: clone M-T310 A;Accession: S19973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment) c;Speckes: Mus musculus (house mouse) C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000 C;Accession: S19971; S19973
                   F;1-20/Domain: signal sequence *status predicted \cdot F;21-131/Product: Ig light chain V region *status
                                                                                                                                                                                     A; Reference number: PH1224; A; Accession: PH1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-112 <WEW>
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A; Residues: 1-112 <WEI>
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                                                            C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-131 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: Structural characterization
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Best Local
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immunoglobulin homology < IMM>
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91.9%;
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Pred. No. 3.1
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Pred. No. 2e
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C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin C:Keywords: heterotetramer; immunoglobulin F:16-94/Domain: immunoglobulin homology <IMM>F:23-92/Disulfide bonds: #status predicted
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A;Residues: 1-111 <WEID
C;Complex: An immunoglobulin heterotetramer subunit consists of two ide
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
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KVMS69
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A; Accession: D01937
A; Molecule type: protein
A; Residues: 1-110 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                               R; Weigert, M.; Gatmaitan, Nature 276, 785-790, 1978
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ittle: Rearrangement of genetic information may produce immunoglobulin Reference number: A93204; MUID:79073152; PMID:103003
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Best Local
                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  kappa chain V region (PC7210) - mouse
Species: Mus musculus (house mouse)
Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
Accession: D01937; A01937
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 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                    DIVLTQSPASLAVSLGQRATISCKASQSLDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                          GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
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91.0%;
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                                                                                                                                86.8%;
                                                                                                              4; Mismatches
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                                                                                                                                  Score 505; DB 1; Pred. No. 9.4e-39;
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Pred. No. 3.8e-40;
4; Mismatches 5;
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                 RESULT 10
S19972
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S19976
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F;16-94/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-112 <WEI>
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A; Accession: S19976
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Ig kappa chain
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 (M-T321) - mouse (fragment)
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4; Mismatches 8
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Pred. No. 1.3e-38;
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related A;Reference number: A93822; MUID:79012520; PMID:99744
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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                                                                         GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                        DIVLTQSPASLAVSLGQRATISCKASQSLDYDADSYMHWYQQKPGRPPKLLIYAASNLES
                                                                                                                                                                           DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCOOSIQDPYTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riethmueller, G.; Weiss, E.M.; Rieber, MBL Data Library, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-Feb-1995 #text_change
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Ig kappa chain V region (PC7175) - mouse (tentative sequence) C:Speciles: Mus musculus (house mouse) C:Date: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_chanc:Accession: B01938; A01938
R:Weigert, M.: Gatmaitan, L.: Loh, E.: Schilling, J.: Hood, L. Nature 276, 785-790, 1978
                                                                                                                                                                                                                                     RESULT 12
KVMS75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
C:Accession: S19972
R:Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A; Molecule type: protein A; Residues: 1-111 <WEI>
                                     A; Reference number: A93204; A; Accession: B01938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X51854; NID:g55397; PIDN:CAA36147.1; PID:g930231 C;Superfamily: Immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C:Accession: S09966
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                                                                                  A; Title:
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A; Residues: 1-111 <REI>
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A; Residues: 1-112 <WEI>
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Best Local :
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                                                       Rearrangement of genetic information may produce immunoglobulin nce number: A93204; MUID:79073152; PMID:103003
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84.7%;
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Pred. No. 5.5
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                                                                                                                                                                  30-Jun-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.5e-36;
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C;Complex: An immunoglobulin heterotetramer subunit consists of two hain disulfide bonds. In some cases, such as IgA and IgM, the subunit C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer
                                                                                                                                                            A;Reference number: A93204; MUID:79073152; PMID:103003
A;Acssion: A01938
                                                                                                                                                                                                                                                                            Ig kappa chain V region (PC6684) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
C;Accession: A01938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>F;23-92/Disulfide bonds: #status predicted
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C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
C;Accession: CO1938; A01938
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
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F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
                                                                                                                          A; Molecule type: protein A; Residues: 1-111 <WEI>
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85.6%;
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Pred. No. 6.
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Pred. No. 1.2e-35;
                                                                                                                                                                                                                                                            E.; Schilling,
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A:Molecule type: DNA
A:Residues: 1-112 <KIM>
A:Residues: 1-112 <KIM>
A:Experimental source: cell line Ex-3C7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted
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S45715
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Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A. BS Lett. 346, 246-250, 1994

BS Lett. 346, 246-250, 199
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C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
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Pred. No. 1.8e-34;
6; Mismatches 13;
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P0163	1 KV2G_MOUSE	113	57.2	333	w
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P1813	1 KV3M_HUMAN	129	57.7	336	٠,
P0443	1 KV1W_HUMAN	129	58.0	337.5	-

ALIGNMENTS

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InterPro; IPR007110; Ig-like InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1 SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1
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PIR; B01937; KVMS83.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY - DETERMINING - 3.
FRAMEWORK - 4.
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21-JUL-1986
15-JUL-1999
                                                       diversity.";
Nature 276:785-790(1978).
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SEQUENCE
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SMART; SM00406; IGV;
PROSITE; PS50835; IG.
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Mus musculus (Mouse).
                                                                                         MEDLINE-79073152; PubM
Weigert M., Gatmaitan
                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                  KV30_MOUSE
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DOMAIN
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HSSP; P80362; 1WTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
19 kappa chain V-III region PC 6308.
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                                                                               Weigert M., Gatmaitan L., Loh E., Schillir Rearrangement of genetic information may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro;
      c; C01937; KVMSO8.
p; P80362; IWTL.
serpro; IPR007110; Ig-like.
erpro; IPR003006; Ig_MHC.
erpro; IPR003596; Ig_v.
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                          PubMed=103003;
itan L., Loh E.,
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Rodentia;
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Last annotation update)
region PC 7043.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                    Score 527.5;
Pred. No. 7.2e
2; Mismatches
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                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                              7A5FCB586C306D29 CRC64;
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RESULT 4
KV3Q_MOUSE
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Matches 101
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Best Local S
Matches 102
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Inter; IPKVV--
Interp; PF00047; 19; 1.
PFam; PF000406; IGv; 1.
SMART; SM00406; IGV; 1.
SMART; PS50835; IG_LKE; 1
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Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
NCBI_TaxID=10090;
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InterPro;
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DOMAIN
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7769.
                                                                                                                                  SEQUENCE
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MEDLINE-79073152; PubMed-103003;
MEDLINE-79073152; PubMed-103003;
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                                                                  101;
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E; PS50835; IG_LIKE;
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                                                                                   Similarity
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); IPR003596; Ig_V.
)0047; 19; 1.
00406; IG.
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obulin V
GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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Rodentia;
                                                                                                                                  12011 MW;
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91.0%;
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Pred. No. 3.6e
4; Mismatches
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Pred. No. 1.8e
2; Mismatches
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BY SIMILARI
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
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Sciurognathi;
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                                                                                                                                  6FAA345279356829 CRC64;
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hi; Muridae;
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                                                        V3L_MOUSE

D KV3LMOUSE STANDARD; PF
C P01664;
C P01664;
T 21-JUL-1986 (Rel. 01, Created)
T 21-JUL-1986 (Rel. 01, Last seque
T 15-JUL-1999 (Rel. 38, Last annot
E Ig kappa chain V-III region CBPC
E Ig kappa chain V-III con CBPC
E Uskaryota; Metazoa; Chordata; CC
C Mammalia; Eutheria; Rodentia; SC
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Best Local Similarity
Matches 100; Conser
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P01668;
21-JUL-1986
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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InterPro; IPR003006;
InterPro; IPR003596;
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PIR; D01937; KVMS10.
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15-JUL-1999
 MEDLINE-79012520; PubMed-99744;
                   SEQUENCE
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MEDLINE-79073152; PubMed-103003;
Loh E.,
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-JUL-1999 (Rel. 38, Last a
kappa chain V-III region
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; Ig_MHC.
; Ig_v.
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region PC 7210.
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90.1%;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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    RESULT 7
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InterPro; IPR003006; I
InterPro; IPR003596; I
InterPro; IPR003596; I
Pram; PR00047; 19; 1
SMART; SM00406; IGv; 1
PROSITE; PS50835; IG_L
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21-JUL-1986
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DOMAIN
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PIR; B01938; KVMS75.
HSSP; P01679; 2FBJ.
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P01671;
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Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A
                                                                                                                                                                                                                                                                               Weigert M.,
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InterPro; IPR003006;
InterPro; IPR003596;
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PS50835; IG_LIKE;
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PS50835; IG
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Pred. No. 1.86
2; Mismatches
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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Sciurognathi;
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P01670;
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HSSP; P80362; 1WTL.
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Mammalia; Eutheria; Rodentia;
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Mus musculus (Mouse).
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P01672;
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                STANDARD;
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information
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                   Score 470.5; DB 1
Pred. No. 3.4e-40;
4; Mismatches 1:
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Pred. No. 1.7
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                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                        MEDLINE-79073152; PubMed-103003; MEDLINE-79073152; PubMed-103003; Loh E.,
                                                                                                                                                                                      21-JUL-1986
21-JUL-1986
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 6684.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalla; Eutheria; Rodentia; Sciurognathi; M
NCBI_TaxID=10090;
                                                   Nature
[2]
                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
        SEQUENCE (TEPC 111).

MEDLINE-79012520; PubMed-99744;

McKean D.J. Bell M., Potter M.;

"Mechanisms of antibody diversity:
                                                           diversity.";
Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE-79073152; PubMed-103003;
MEDLINE-79073152; PubMed-103003;
related
                                                                             weigert M., Gatmaitan L.,
"Rearrangement of genetic
                                                                                                                                                                                                                               KV3H_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A01938; KVMS84.
HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diversity
                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Rearrangement of
                                                                                                                                                                          -JUL-1986 (Rel. 01, Created)
-JUL-1986 (Rel. 01, Last sequence update)
-JUL-1999 (Rel. 38, Last annotation update)
kappa chain V-III region PC 3741/TEPC 111.
                                                                                                                                                                                                                                                                               1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                                                                   93;
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mouse
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kappa
                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                              Chordata;
Rodentia;
variable regions
                                                                                                                                                                                                                                                                                                                                                                           80.5%;
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information may produce immunoglobulin
                                                                                 Loh E., Schilling J.,
information may produc
                                                                                                                                                                                                                                                                                                                                                                 Score 468.5;
Pred. No. 5.4e
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                              Craniata; Vertebrata; Sciurognathi; Muridae;
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        multiple
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         genes
                                                                                           Hood L.E.;
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          encode
                                                                                  immunoglobulin
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; Murinae; Mus
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          structurally
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Best Local S
Matches 90
                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
       DOMAIN
DISULFID
NON_TER
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21-JUL-1986
21-JUL-1986
15-JUL-1999
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NON_TER
SEQUENCE
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DOMAIN
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DOMAIN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                   Weigert M., Gatmaitan L., "Rearrangement of genetic diversity.";
                                                                                                                                                                                    SEQUENCE:
MEDLINE-79073152; PubMed-103003;
MEDLINE-79073152; PubMed-103003;
                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
1: MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
PIR, A93204; KVMS37.
HSSP; P01679; 2FBJ.
                                   DOMAIN
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                                                                      DOMAIN
                                                                               DOMAIN
                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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                                                                                      Immunog lobul in
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                                                                                                                                                            Nature
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-JUL-1986 (Rel. 01, Last sequence up-
-JUL-1999 (Rel. 38, Last annotation
kappa chain V-III region PC 4050.
                                                                                                                                                   P01679; 2FBJ
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Rodentia;
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81.1%;
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information
                        FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Pred. No. 1.1e-38;
7; Mismatches 13
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                 ВУ
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COMPLEMENTARITY-DETERMINING-2
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                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                    PRT;
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39D87619313453CB
                 SIMILARITY.
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ID KV3J_MOUSE
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Best Local
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Best Local :
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 21-JUL-1986
21-JUL-1986
15-JUL-1999
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DOMAIN
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InterPro;
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MEDLINE=79073152; PubMed=103003;

MEDLINE=79073152; PubMed=103003;
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HSSP; P01679; 2FBJ.
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Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig kappa chain V-III region PC 2485/PC
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P01673;
                                                         P01662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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"Rearrangement of genetic
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SCELLANEOUS: THE PC
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92; Conserv
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                                                                                                                                                                     GVPARFSGSGSGTDFTLNIQPVEEEDAAIYYCQHSRELPLTFGAGTKLELK
                                                                                                                                                                                        GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                          DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASSLES
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IPR003006;
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   38,
01,
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Rodentia;
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Ig_MHC.
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Created)
Last sequence up
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4; Mis
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Pred. No. 1.3
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Pred. No. 1.
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                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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2485/PC 4039.
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                    update)
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RESULT 14
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SEQUENCE (ABPC 22).
MEDLINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
"Mcchanisms of antibody diversity: multiple genes
"hechanisms of antibody diversity: multiple genes
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
MEDLINE-7823587; PubMed-98179;
Burstein Y., Schechter I.;
"Primary structures of N-terminal extra peptide segments linked
the variable and constant regions of immunoglobulin light chain
precursors: implications on the organization and controlled
expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
                                                                                                                                                                   Mammalla; Eutherla; Rodentla; NCBI_TaxID=10090;
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                                                                                                                       SEQUENCE OF 1-35.
MEDLINE-78235887;
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Mammalia; Eutheria; Rodentia;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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Pred. No. 4.
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DISULFID
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SEQUENCE
                                     kappa chains.";
Science 155:465-467(1967).
Science TANEOUS: THIS IS
                                                                            MEDLINE=67056897;
Gray W.R., Dreyer
                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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KV3C_MOUSE
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"Mouse immunoglobulin chains. Pattern of sequence kappa chains with limited sequence differences.";

Biochemistry 12:760-771(1973).
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SEQUENCE OF 21-131.
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HSSP; P01679; 2FBJ.
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InterPro; IPR003006; Ig_MHC.
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                     between
                                                                                                                                        Euteleostomi;
                                                                                                                              Murinae;
                                                                                                                                                                                                                                                                                                                                                          131;
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                                                                     mouse
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                 80
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DR Pfam: PF00047; ig: 1.

DR SMART; SM00406; IGv: 1.

DR PROSTTE; PS50835; IG_LIKE; 1.

ET DOMAIN

THE DOMAIN

THE DOMAIN

S4 38 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN

FT DOMAIN

FT DOMAIN

S4 50 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN

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S4 50 COMPLEMENTARITY-DETERMINING-3.

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S4 50 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN

S5 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN

S6 SEQUENCE

THE TOMAIN

S6 SEQUENCE

THE TOMAIN

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ob time : 24 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                    tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arched:
                                                                         SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
7: sp_mage:*
10: sp_plant:*
11: sp_rodent:
12: sp_vius:*
13: sp_vertebr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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582
1 DIVLTNSPASLAVSLGQRAT.....CQLCNEDPPTFGAGTKLELK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830525 seqs, 258052604 residues
sp_phage:*
sp_plant:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_vertebrate:*
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sp_vertebrate:*
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sp_bacteria:*
sp_fungi:*
                                                                                                                                                                       sp_mammal:*
sp_mhc:*
                                                                                                                                                           sp_organelle:*
                                                                                                                                                                                                         sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                         830525
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	G	4	w	2	_	No.	Result
330	334	334	335	335	338.5	340	341	341.5	341.5	342	346	348.5	352.5	413.5	467.5	Score	
56.7	57.4	57.4	57.6	57.6	58.2	58.4	58.6	58.7	58.7	58.8	59.5	59.9	60.6	71.0	80.3	Match I	Query
114	239	238	112	109	108	112	107	234	108	238	109	108	108	103	111	Length I	
11	4	11	11	4	4	11	4	4	4	11	4.	4	4	11	11	DB	
Q8K1F1	OSTCD0	Q99M37	Q8K1F3	Q9UL85	Q9UL83	Q8K1F2	Q96SA9	Q8NEK1	Q9UL77	Q8VCI6	Q9UL78	Q9UL79	Q9UL70	Q9JL80	Q920E9	Ħ	
Q8k1f1 mus musculu	OStadO homo sapien	099m37 mus musculu	Q8k1f3 mus musculu	Q9ul85 homo sapien	Q9ul83 homo sapien	Q8klf2 mus musculu	Q96sa9 homo sapien	Q8nek1 homo sapien	Q9ul77 homo sapien	Q8vci6 mus musculu	Q9u178 homo sapien	Q9u179 homo sapien	Q9u170 homo sapien	Q9j180 mus musculu	Q920e9 mus musculu	Description	

4 4 5	43	42	41	40	39	38	37	36	35	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
280 279.5	283.5	286.5	288.5	288.5	289.5	291.5	293.5	294.5	299.5	301.5	304.5	305	305	305.5	306.5	308	309.5	311	311	312	313.5	314	321.5	324	325	325.5	327
48.1 48.0	48.7	49.2	49.6	49.6	49.7	50.1	50.4	•	•	51.8	•	52.4	52.4	52.5	52.7	52.9	53.2	53.4	53.4	•	•	•	•	•	55.8	•	•
148	101	97	234	116	107	109	298	234	233	99	218	235	104	234	234	134	107	112	109	239	214	106	108	239	107	114	239
6	11	1	11	4	11	11	11	11	片	11	11	11	11	11	11	H	11	11	4	11	二	ഗ	11	4	4	4	11
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Q8k122 mus musculu Q9n0w5 oryctolagus		mus	mus	homo	Q9jl84 mus musculu	Bum	Rus	Rum	Q91ws9 mus musculu	Bum	Bum	Q91w12 mus musculu	mus	mus	mus	mus	Bum	Bum	homo	mus	Q9rla5 mus musculu	Q9u410 schistosoma	mus	Omo	Q9u181 homo sapien	Q9u180 homo sapien	Q8vc55 mus musculu

ALIGNMENTS

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1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59	Query Match 80.3%; Score 467.5; DB 11; Length 111; Best Local Similarity 83.8%; Pred. No. 1.5e-43; Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	O920F9 PRELIMINARY: PRT: 111 AA

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PRESENTE SERVICE SERVI
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Best Local S
Matches 80
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                          Q9UL70;
Q9UL70;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JL80;
      Clin.
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SEQUENCE
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(Fragment).
(Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; /
                                                                                                      MEDLINE-98277139; PubMed-9614934; MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20448942; PubMed-10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 23, Last annotation update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                     Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis"
                                                                                            Wu X., Liu B.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF206021
HSSP; P80362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BALB/C;
                                                                                                                                                                                                       NCBI_TaxID-9606;
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                                              etus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiac myosin."
      Immunol.
AF035044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. Immun. 68:5803-5808(2000).
AF206026; AAF69324.1; -.
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      AAD56280.1;
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77.78;
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Pred. No. 1.1e
10; Mismatches
                           87:184-192(1998)
                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                    Kalis
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                                                                       and
                                                                                                                    S.M.,
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RESULT 5
Q9UL78
ID Q9UL78
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Matches 68
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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01-MAY-2000
01-MAY-2000
01-MAR-2003
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NON_TER
SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
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Homo Sapiens (Human).
Homo Sapiens (Human).
'``rvota; Metazoa; Chordata; '
'``rvota; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clin. Immunol. Immunopathol. EMBL; AF035035; AAD56271.1; HSSP; P01607; 1REI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.
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TE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Liu B.,
, D.C.;
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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108 /
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    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                     AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108
11633 MW;
                                                                                                                                                                                                                                                                                                                                                                                     108
11787 MW;
                                                                                                                                                                                                                                                                                                                    59.9%;
61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.6%;
61.3%;
                                                                                                                                                                                                                                                                                               15;
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                                                                                                                                                                                                                                                                                                                    Score
Pred.
    PRT;
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DR DR DR DR DR DR DR DR SQ
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1
SMART; SM00406; IGv; 1.
PR0STTE; PS50835; IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                              DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK
                                               DIVMTQSPSLLSASTGDRVTISCRMSQGI----SSYLAWYQQKPGKAPELLIYAASTLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBLrel. 13, Created)
EMBLrel. 13, Last sequence update)
EMBLrel. 23, Last annotation update)
immunoglobulin light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig-like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 352.5; DB 4
Pred. No. 5.7e-31;
6; Mismatches 22
                                                                                                                                                                                                                                                                                      87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                 DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B7BEDC3E41FCCA37 CRC64;
                                                                                                 Mismatches
                                                                                                            348.5;
No. 1.6
                                                                                                                                                                                                                                                                                                              rheumatic
                                                                                                                                                                                                                                                                                                                                      Kalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                               5; DB 4;
1.6e-30;
hes 23;
                                                                                                                                                                                                                                                                                                                                     N. N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                               carditis
                                                                                                                                                                                                                                                                                                                                      Berney
                                                                                                 Indels
                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                         108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
                                                                                                 5
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 107
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                 56
                                                                         59
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RESULT
Q8VCI6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRIA RRA
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 69
          Query Match
Best Local
  Matches
                                                              Strausberg R.;
Submitted (DEC-2001) to the EMEMBL; BC019760; AAH19760.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                               Q8VCI6 PRELIMINARY; PR
Q8VCI6;
01-MAR-2002 (TrEMBLrel. 20, Crea
01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 26.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
PROSITE; PS50835; IG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                      PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 238 AA; 26224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Immunol. Immu
EMBL; AF035036; AAI
HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                TISSUE=Colon;
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu X., Liu B.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-98277139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myosin-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL78;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                             58 GIPDRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                60
 l Similarity
68; Conserv
                                                                                                                                                                                                                                                                                                                                   \vdash
                                                                                                                                                                                                                                                                                                                                                     \mathbf{\mu}
                                                                                                                                                                                                                                                                                                                                                                        69;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                             109
109 A
 Conservative
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunopathol.
AAD56272.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBLrel. 13, Created)
EMBLrel 13, Last sequence update)
EMBLrel. 23, Last annotation update
immunoglobulin light chain variab
                                                                                                                                                                                                                                                                                                                                                                                                                                      [Gv; 1.
IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       der
                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                             11646 MW;
          58.8%;
60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merwe
 14;
Score 342; DB
Pred. No. 2.2e
14; Mismatches
                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                      Score 346; DE
Pred. No. 3e-3
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87:184-192(1998).
                                                                                                                                                                    Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            5F675C52EC7EE197
                                     35EC08E3DE5414AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalis N.N.,
                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                                                                                                3e-30;
                                                                                                                                                                              Vertebrata;
         DB 11;
.2e-29;
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                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n update)
variable
                   11;
                                                                                                                                                                     Muridae;
                                                                                                                                                                                                                                                                                                                                                                                         4,
                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carditis and normal
 28;
                                                                                                               databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berney
                                                                                                                                                                                                                                                                                                                                                                                        Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                  Length
 Indels
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reg
                                                                                                                                                                      Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tion
                    238;
 2
                                                                                                                                                                      Mus
Gaps
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                     59
2;
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                                                                                                                                                                                               Q
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                                                                                                                                                                                                                                    QΥ
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                                                                                                                                                   RESULT 8
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                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              Clin. Immunol. Immunopathol. EMBL; AF035037; AAD56273.1; HSSP; P01607; 1REI.
                                                       Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pi
                                                                                          01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL77;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; SMART; SM00406; IG;
                   TISSUE=Lung;
                            SEQUENCE FROM
                                               NCBI_TaxID=9606;
                                                                                                                        Q8NEK1;
                                                                                                                                  Q8NEK1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu X., Liu B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=98277139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UL77
                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                            fetus.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                              D.C.
                                                                                                                                                                                57
                                                                                                                                                                                                 60
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                                                                                                                                                                                                                                                         67; Conserv
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                                                                                                                                                                                                                                                                                                                         PS50835;
                                                                                                                                                                                                                                                                                                                                                  IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                             108
108 A
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                             AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Van
                                                                                                                                                                                                                                                                                                                                  IGV;
                                                                                                                                                                                                                                                                                                                         IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                        Primates;
                                                                 Chordata;
                                                                                                                                                                                                                                                                                              11738 MW;
                                                                                                                                                                                                                                                                  58.7%;
the
                                                                                            22,
23,
                                                                                                                                                                                                                                                        17;
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DR RC SISCE HERO SISCE
Strausberg R.;
Submitted (JUN-2002) to the
EMBL; BC030813; AAH30813.1;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Myosin-reactive immunoglobulin light chain variab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIQMTQSPSSLSASVGDRVTITCRASQSI----SSYLNWYQQKPGKAPNLLIYAASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9614934;
n der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 341.5;
Pred. No. 9.2e
17; Mismatches
                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                               Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
                                                                                                                                                                                                                                                                                    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               z.
z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n update)
variable
                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                        databases
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Best Local S
Matches 66
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SMART; SM00406; IG: 1.
SMART; SM00406; IG: 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 234 AA.
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InterPro;
InterPro;
  Q8K1F2
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; "Molecular analysis of polyreactive monoclonal antibodies from Theumatic carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-98375893; PubMed-9712075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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|| :| ||:||: ||: ||:||:||:||:||:||
DIQMTQSPSSLSASVGDRVTITCRASQSI----SSYLNWYQQKPGKAPKLLIYAASSLQS
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; IPR003597; Ig_cl.
; IPR003006; Ig_MHC.
; IPR003596; Ig_v.
                                                                                                                                              GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ-SYSTLTFGGGTKVEIK
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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107
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  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                               11520 MW;
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                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                          Score 341; DB 4
Pred. No. 1e-29;
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  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                               4BB43E9C5B577F16 CRC64;
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No. 2.4
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                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                             Length 107;
                                                                                                                                                                                                                                                                                                     Indels
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RESULT 11
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Best Local
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01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
Anti-VIPase light chain v
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01-MAY-2000
01-MAR-2003
PROSITE;
NON_TER
NON_TER
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UL83;
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NON_TER
SEQUENCE
                                                                                                                                                                             EMBL;
HSSP;
                                                                   InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C: TISSUB-Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Pau
"Innate proteolytic antibodies: Failed D-VIPase response to the
entantiomer of VIP and identification of L-VIPase VL domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-virase Mouse).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF516283; AAM64201.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/c; TISSUE-Hyperimmunized
                                                                                                                                InterPro;
                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                 fetus.
                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin-reactive
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                                                                                                                                                                           Immunol. Immunopathol. 8 AF035031; AAD56267.1; -- P80362; IWTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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                                               PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELK
                                                                                                                                IPR007110;
IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) (TrEMBLrel. 13, () (TrEMBLrel. 13, ) (TrEMBLrel. 23, )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
    108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBLrel. 13, Last sequence update)
EMBLrel. 23, Last annotation update)
immunoglobulin light chain variable
                                               IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11953 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.4%;
                                                                                                                                   Ig_MHC
                                                                                                                                                     Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22, Created)22, Last sequence update)23, Last annotation update)variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 340;
Pred. No. 1
                                                                                                                                                                                                                        87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4716B87FADB543ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                   in rheumatic carditis
                                                                                                                                                                                                                                                                                                              Kalis
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.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                              z. z. ,
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                                                                                                                                                                                                                                                                                                              Berney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                      and normal
                                                                                                                                                                                                                                                                                                                S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 S.;
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RESULT
Q8K1F3
ID Q8K1F3
OR Q8K1F3
OT Q8
DT 01
DT 01
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Q9UL85
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
01-OCT-2002 (TrEMBLrel. 22, Created 01-OCT-2002 (TrEMBLrel. 22, Last se 01-MAR-2003 (TrEMBLrel. 23, Last an Anti-VIPase light chain variable re Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Crani Mammalla; Eutheria; Rodentla; Sciur NCBI_TaxID=10090;
                                                           Q8K1F3;
Q8K1F3;
Q1-OCT-2002
Q1-OCT-2002
Q1-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL85;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Myosin-reactive immunoglobulin kappa chain v
                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UL85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF035029; AA
HSSP; P80362; 1WTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                     PF00047; 1g; 1.
; SM00406; IGv; 1.
TE; PS50835; IG_LIKE;
                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunol. Immunopathol. AF035029; AAD56265.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                      67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG
                                                                                                                                                                                     IPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPP-TFGAGTKLELK
                                                                                                                                                                                                                      EIVMTQSPATLSVSPGERATLSCWASQSI---SSNLAWYQQKPGQAPRLLIYGASTRATG
                                                                                                                                                                                                                                    DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG
                                                                                                                                                                       IPARFSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPARFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIVMTQSPATLSVSPGERATLSCRASQSV---SSNLAWYQQKPGQAPRLLIYCASTRATG
                                                                                                                                                                                                                                                                                                                                                                                             IPR003596;
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                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                           Ig-like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                               57.6%;
                                                                                                                                                                                                                                                                                                                       11761 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                      Created)
                                                                                                                                                                                                                                                                                 Score 335; DB 4;
Pred. No. 4.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 338.5; DB Pred. No. 2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          87:184-192(1998)
            Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                     FB1E43E7C7AFACCC CRC64;
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                                                sequence up
annotation
region (Fra
                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                              112
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                                                ce update)
tion update)
(Fragment).
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               Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carditis
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                                                                                                                                                                                                                                                                                            Length 109;
                                                                                                                                                                                                                                                                      Indels
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             Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
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Q99M37
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                                                                                                                        Query
Best I
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Best Local
                                                                                                           Matches
                                                                                                                                                   PROSITE; PS50835; IG_LIKE; 2
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (JAN-2001) to the Submitted EMBL; BC002035; AAH02035.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul "Innate proteolytic antibodies: Failed D-VIPase response to the entantiomer of VIP and identification of L-VIPase VL domains."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF516282; AAM64200.1; -.
                                                                                                                                                                                                                     InterPro; IPR007110; 1
InterPro; IPR003006; 1
InterPro; IPR003596; 1
Pfam; PF00047; 1g; 2.
                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical 26.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q99M37;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/c; TISSUE-Hyperimmunized spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                         Local
                                                                                                                                    Match
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T; SM00406; IGv; 1.
T; SM05406; IG_LIKE; ?
                                                                                                                                                                                                                                                                     P01679;
             80
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                                                                                                           . Similarity 67; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG
                         SGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                            DIVLTNSPASLAVSLGQRATISCKASQSVDY-DGDSYM-WYQQKPGQPPKLLTYAASNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPARFSGSGSGTSYSLTISSMEAEDAATYYCQQYHSYPYTFGGGTKLEIK
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             SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003599; Ig.
                                                                                                          57.4%;
nilarity 59.8%;
Conservative 1
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112 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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1, 12017 MW;
                                                                                                                                                            26344 MW;
                                                                                                                                                                                                                               Ig-like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.6%;
60.9%;
                                                                                                          ; Score 334; DB 11;
; Pred. No. 1.6e-28;
17; Mismatches 26;
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                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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Pred. No. 5e-29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                            FB2B06A0B801330A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                           Indels
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; Murinae; Mus
                                                                                                           <u>ب</u>
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               131
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RESULT 15
Q8TCD
ID Q8TCD
ID Q8TCD
AC Q8TCD
DT 01-JU
DT 01-JU
DT 01-MA
DE HYPOT
OS HOMO
OC EUKAr
OC Mamma
OX NCEIL-
RN [1]
RP SEQUE
RC TISS(
RA Stran
CRL Submi
DR Intel:
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Search completed: September 13, 2003, 07:54:30 Job time : 89 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

C TISSUE-Lung;
Strausberg R.;
L Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC022362; AAH22362.1; -.
R InterPro; IPR003706; Ig_MHC.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 2.
Pfam; PF00047; 1g; 2.
R PROSITE; PS00835; IG_MHC; 1.
R PROSITE; PS00290; IG_MHC; 1.
W Hypothetical protein.
SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03B71D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 57.4%; Score 334; DB 4; Length 239; Best Local Similarity 58.0%; Pred. No. 1.6e-28; Matches 65; Conservative 18; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8TCD0
                                                                                                                                                                                                                                                                                                                                                                                  1 DIVLTNSPASLAVSLGQRATISCKASQSVDY-DGDSYM-WYQQKPGQPPKLLTYAASNLE 58 | 1:1:1 | 1 | 1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:1|1 | 1:
                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                   59 SGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQUCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWPSTFGQGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

19

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
            BLOSUM62
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582
1 DIVLTNSPASLAVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541936 seqs, 145912426 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       September 13, 2003, 07:55:26; Search time 54 Seconds (without alignments) 297.229 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA: *
                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES
0,

Result No.

Result	Score	Query Match	Length DB		ID	Description
_	582	100.0	110	11	US-09-759-112A-24	Sequence 24, Appl
Ŋ	537.5	92.4	132	10	US-09-879-461-2	Sequence 2, Appli
ω	528.5	90.8	238	15	US-10-216-484-11	
4	526.5	90.5	238	10	US-09-903-327A-4	Sequence 4, Appli
U	505.5	86.9	112	15	US-10-194-975-115	۳.
σ	503.5	86.5	106	9	US-09-802-077-6	Sequence 6, Appli
7	503.5	86.5	106	9	US-09-802-096-6	Sequence 6, Appli
8	503.5	86.5	106	11	US-09-925-179-6	Sequence 6, Appli
9	491.5	84.5	111	9	US-09-802-077-2	Sequence 2, Appli
10	491.5	84.5	111	9	US-09-802-096-2	Sequence 2, Appli
11	491.5	84.5	111	11	US-09-925-179-2	Sequence 2, Appli
12	490	84.2	112	12	US-10-160-506-81	Sequence 81, Appl
13	487.5	83.8	238	15	US-10-216-484-54	
14	485.5	83.4	111	9	US-09-920-171-5	
15	485.5	83.4	111	12	US-10-113-996-5	Sequence 5, Appli

476.5 81.9 238 15 US-10-216-484-52 475.5 81.7 238 15 US-10-216-484-109 475.5 81.7 271 12 US-10-207-655-12 475.5 81.7 271 12 US-10-207-655-12 475.5 81.7 271 12 US-10-207-655-12 475.5 81.7 271 15 US-10-207-655-12 475.5 81.7 271 15 US-10-207-655-12 475.5 81.7 271 15 US-10-207-655-12 475.5 79.6 131 10 US-09-879-461-14 481.5 77.9 112 10 US-09-114-886-80 453.5 77.9 218 15 US-10-171-452A-53 453.5 77.9 218 15 US-10-171-452A-57 453.5 77.9 238 15 US-10-171-452A-57 453.5 77.9 238 15 US-10-171-452A-58 453.5 77.9 238 15 US-10-171-452A-58 453.5 77.9 238 15 US-10-171-452A-69 468.5 77.1 112 10 US-09-144-886-84 468.5 77.1 112 10 US-09-144-886-84 468.5 77.1 129 15 US-10-153-271-2 468.5 76.7 129 15 US-10-153-271-2 468.5 76.7 129 15 US-10-153-271-2 468.5 76.7 132 10 US-09-974-052-13 468.5 76.7 110 11 US-09-974-052-13 468.5 76.2 113 10 US-09-974-551-13 468.5 76.0 113 10 US-09-974-551-13 468.5 76.0 113 10 US-09-974-551-13 468.5 76.0 113 10 US-09-974-551-13
115 0 0 0 0
g g g
US-10-216-484-52 US-10-216-484-109 US-10-207-655-12 US-10-207-655-12 US-09-879-461-18 US-09-879-461-18 US-09-879-461-18 US-09-810-502-37 US-09-114-486-80 US-10-171-452A-45 US-10-171-452A-45 US-10-171-452A-57 US-10-171-452A-58 US-10-171-452A-58 US-10-171-452A-58 US-10-171-452A-58 US-10-171-452A-58 US-10-171-452A-59 US-10-180-881-881 US-10-180-89 US-10-180-881-81 US-09-974-052-13

ALIGNMENTS

RESULT 1 US-09-759-112A-24

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NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 110
TYPE: PRT
RESULT 2
US-09-869-461-2
; Sequence 2, Application US/09879461
; Publication No. US20020193575A1
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                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: mouse US-09-759-112A-24
                                                                                                                                                                                                                                                                Query Match 100.0%; Score 582; DB 11; Best Local Similarity 100.0%; Pred. No. 1.8e-49; Matches 110; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/09759112A Publication No. US20030100741A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mueller, Sybille
APPLICANT: Mobler, Heinz
APPLICANT: Kohler, Heinz
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LI
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTI
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                        Length 110;
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                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                              60
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8
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                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-879-461-2
                                                                                                                                                                                                                       Sequence 11, Application US/10216484 Publication No. US20030103976A1
                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
                                                       APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Holmes, Stephen D.
Gross, Mitchhell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 132 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corporate Intellectual Property, UW2220 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.48;
93.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 537.5; DB 10
Pred. No. 4.7e-45;
1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4
LENGTH: 238
TYPE: PRT
                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 11
                                                                                                                    Sequence 115, Application US/10194975 Publication No. US20030039649A1
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                         APPLICANT: Foote, Jefferson TITLE OF INVENTION: Super Humanized Antibodies FILE REFERENCE: 501231.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DELLVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Li, Erguang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES
TITLE OF INVENTION: GENE
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
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TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                       103;
                                                                                                                                                                                                                                            81 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQTNEDPWTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                 60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                      21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES, 80
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Similarity 92.8%;
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92.8%;
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Pred. No. 6.8e-44;
Pred. No. 6.8e-44;
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Pred. No. 1.1e-43;
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; ORGANISM: Mus sp.
US-10-194-975-115
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Sequence 6, Application US/09802096
Patent No. US20010038839A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing
FILE REFERENCE: P0718P2C3US
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PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 115
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LENGTH: 106
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Best Local
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718p2c2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus 09-802-077-6
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PRIOR FILING DATE: 1992-05-07
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Pred. No. 5.2e-42;
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                 Allergic
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                   Disorders
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CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: CT/US92/06860
PRIOR APPLICATION NUMBER: CT/US92/06860
PRIOR FILING DATE: 1992-08-14
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Best Local
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Best Local Similarity 93.4%;
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-JgE Antibodies (as
FILE REFERENCE: P0718P2C1D1C1US
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1991-08-14
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TYPE: PRT
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TYPE: PRT
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1 Similarity 93.4%;
99; Conservation
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Conservative
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                                                                        Score 503.5; DB 11;
Pred. No. 7.6e-42;
Prematches 6;
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60 GIPARESGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGT 105

GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPFTFGAGT 106

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                                                              ; ORGANISM: Mus musculus US-09-802-096-2
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US-09-802-096-2
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CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR APPLICATION NUMBER: US 07/879,495
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                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 2
LENGTH: 111
TYPE: PRT
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PRIOR FILING DATE:
PRIOR APPLICATION NU
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended FILE REFERENCE: P0718P2C3US
CURRENT ETLING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-08-14
PRIOR FILING DATE: 1994-08-14
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LENGTH: 111
Query Match
Best Local
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TITLE OF INVENTION: Method of Treating Allergic Disorders
FILE REFERENCE: P0718P2C2US
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APPLICANT: Presta, Leona:
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PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
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  Similarity
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Pred. No. 1.2e-40;
Score
Pred.
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491.5; DB 9;
No. 1.2e-40;
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                                                                                                                                                                                                                                                                                            Sequence 81, Application US/10160506 Publication No. US20030161832A1 GENERAL INFORMATION:
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Matches
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LENGTH: 111
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NUMBER OF SEQ ID NOS: 128
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
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                                                                                                     CURRENT APPLICATION NUMBER: US/10/160,506
CURRENT FILLING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/324,100
PRIOR FILING DATE: 2001-09-20
                                                                                                                                                                                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECTITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: P0718P2C1DiC1US
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-IgE Antibodies (as
                                                           PRIOR APPLICATION NUMBER: 60/362,612 PRIOR FILING DATE: 2002-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 08/466,163 PRIOR FILING DATE: 1995-06-06
                                                                                                                                                                                         FILE REFERENCE: 10448-162001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 08/405,617 PRIOR FILING DATE: 1995-03-15
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88.3%; Pred. No. 1.2e-40;
3. Mismatches 9;
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Sequence 5, Application US/09920171
Patent No. US20020054878A1
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
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US-09-920-171-5
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FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/99/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: US/99/053,583
PRIOR FILING DATE: 1998-04-01
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LENGTH: 238
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Best Local S
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TITLE OF INVENTION: Improved Anti-IgE Antibodies FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
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APPLICANT: Takahashi, Tohru
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
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Similarity 83.8%;
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Similarity 85.7%;
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Pred. No. 1.7e-40;
7; Mismatches 7;
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             Search completed: September 13,
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Publication No. US20030149244A1
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PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 5
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Best Local
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CURRENT APPLICATION NUMBER: US/10/113,996
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
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ORGANISM: Mus musculus
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97; Conserv
                                                                                                                             1 DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPILLIYAASYLGS
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97; Conserv
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Pred. No. 4.6e-40;
3; Mismatches 10;
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Pred. No. 4.6e-40;
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Title:
Perfect score:
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No.
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Maximum Match 100%
Listing first 45 summaries
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RESULT 1 AAL48660 ID XXX ACC XXXX ACC X Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection; gene; ss. Mus Murine Mab 1F7 light chain coding sequence AAL48660 standard; DNA; 330 Muller S, (IMMP-) IMMPHERON INC 11-JAN-2001; 2001US-0759112 11-JAN-2002; 2002WO-US00927 18-JUL-2002. WO200255668-A2 11-OCT-2002 (first entry) AAL48660; Kohler H; ВР

New polynucleotide encoding a complementarity or framework determining

2002-590668/63

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                                                                                                                                                                complementarity determining region; framework FR; heavy chain; light chain; HIV infection;
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                                                                                                                                                                                                                                                                                                                              ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 330; DB 24;
Pred. No. 2.1e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 4
AAX85884
ID AAX8
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AC AAX8
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Best Local Sim
Matches 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spleen cells from mice immunized with human IL-4 were used to pihybridomas, which were screened for anti-IL-4 MAb secretion. Or clone 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEN7f+ and transformed into E. coli pH5-4hpha. The clones were sequenced (AAQ83490-91), and used for anti-Carrian contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric and humanised IL-4 monoclonal dntibodies (mabs), derifrom high affinity mabs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1993;
14-OCT-1993;
                AAX85884;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DH5-alpha. The clone antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig.1; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-123387/16.
P-PSDB; AAR70189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9507301-AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                      AAX85884 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                               241
                                                                                                                                                                                                                    178
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SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                       CAACAGAAACCAGGACAGCCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                                                                                                                                        ATCTCCTGCAAGGCCAGACCAAAGTGTTGATTATGATGATGATAGTTATATGTG----TGGTAC
                                                                                                                                                                                                                                                                                                                                                     GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                       GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                                                                                                                                                                        GACATTGTGCTGACCCAATCTCCAGCCTTCTTTGGCTGTCTCTAGGGCCAGAGGGCCACC
                                                                                                                                                                    CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
                                                                                                                                                                                                                                          CAACAGAAACCAGGACAGCCAACCCCAAACTCCTATGCTGCATCCAATCTAGAATCT
                                                                                                 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA
                                                                                                                      ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                                                                                                                                            GGGATCCCAGCCAGGTTTAGTGGCAGTGGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                                                                                                                          ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTAC
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0117366.
93US-0136783.
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/*tag=
61..396
/*tag=
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                                      CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 103 C; 103 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                   89.38;
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                                      396
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                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                   Score 294.6;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR
                                                                                                                                                                                                                                                                                                                                                                                                   .2e-81;
                                                                                                  393
                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                    Дb
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Best Local S
Matches 316
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07-SEP-1993;
14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                                                                                               The present sequence encodes the light chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. b. ELISA of circulating endogenous IL-4 levels in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY23767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-429500/36
                                                             178
             238
                                    241
                                                                                  181
                                                                                                          118
                                                                                                                                 121
                                                                                                                                                        61
                                                                                                                                                                                                                               316;
                                                                                                                                                                                 61
                                                                                                                                                                                           1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                                                                                                                          Similarity
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CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
                                                                                  Sp
                                                GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTTGGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC
                                                                                                                                                                                GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTAGGGCAGAGGGCCACC
                                                                                                                                                                                                                                                                             396 BP; 99 A; 103 C; 103 G; 91 T; 0 other;
                                     GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes SD,
                                                                                                                                                                                                                               Conservative
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94.9%;
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Mismatches

Indels

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Gaps

60

120

237 240 177 180 117

297 300 Score 294.6; Pred. No. 2.

; DB 20; .2e-81;

Length

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Chimeric antibody; humanised antibody; IL-4 mediated allergic reactio 
Immunoglobulin E-mediated allergic reaction; allergic rhinitis; 
conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; 
rheumatoid arthritis; host-versus-graft disease; renal disease;
                                     New DNA molecules encoding recombinant antibodies treating IL4-mediated conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain variable region
Fig 1; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                         95US-0483632.
93US-0117366.
93US-0136783.
94WO-US10308.
                                                                                                                                                                                                                                                                                                                                                                                95US-0483632.
                                                                                                                                                                                                           BEECHAM
BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                  Sylvester
                                                                                                                                                                                                           CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL-4 antibody
                                                             useful
                                                               for
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300 237

297

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В
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AAX79519
ID AAX7
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XX 11-A
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XX Anti
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                                                                                                                                      Query Match
Best Local Similarity
Matches 316; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
07-SEP-1993;
14-OCT-1993;
                                                                                                                                                                                                          This sequence encodes the light chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (II4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                          Recombinant IL4 antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                     Gross
                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune
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                118
                                                                                                                                                                                                                                                                                                                                                                                             1999-370482/31
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                                                                                                                                                                                                                                                                                                                                                                                                                     MS,
                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain
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                                                                                                                                                                                                                                                                                                                                                                                   AAY18120
                                   ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC
                                                                                   396 BP; 99 A; 103 C; 103
             CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease;
                                                                                                                                                                                                                                                                                                                                                                                                                     Holmes SD,
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding
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93US-0117366.
93US-0136783.
94WO-US10308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0483636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                  89.38;
94.98;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sylvester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORP.
                                                                                                                                   score 294.6; Pred. No. 2.2e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for murine 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                    DR;
                                                                                                                                              294.6;
                                                                                                                                                                                     G; 91 T;
                                                                                                                                                2e-81;
                                                                                                                                                             ĎВ
                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody.
                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS
                                                                                                                                    Indels
                                                                                                                                                            Length
                                                                                                                                                                                                                    proliferation ases and graft
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                                                                                                                                   Gaps
                                                            117
               177
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                                                                                                                                                                                                                                           RESULT 6
AAZ58690
ID AAZ5
XX AAZ5
XX AAZ5
XX CD4
DT 17-A
XX CD4
XX CD4
XX CD4
XX O7-E
PD 07-E
XX 26-N
XX 26-N
XX APL;
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DR WPI;
DR WPI;
DR WPI;
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DR P-PS
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                                                                                                                                                                                              Query Match
Best Local S
Matches 315
                                                                                                                                                                                                                                                                            The invention provides an antibody having affinity to CD4 antigen. 1 anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the antibody 4H5 L chain fragment encoding
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-091351/08
P-PSDB; AAY59267.
                                                                                                                                                                                                                                            Sequence 333 BP; 87
                                                                                                                                                                                                                                                                   nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                An antibody and the nucleic acid coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                             (ASAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP11332563-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4 antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody
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                                             CAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT
                                                           CAACAGAAACCAGGACAGCCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                              ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTAC
                                                                                                        ATCTCCTGCAAGGCCAAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC
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                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                            Conservative
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94.6%;
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                                                                                                   Query watch
Best Local S
Matches 315
                                                                                                                                                                                    This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence encodes a murine derived protein fragment which is used
                                                                                                                                                                                                                                                                                                                  Disclosure; Page 97-98; 111pp; Japanese
                                                                                                                                                                                                                                                                                                                                          Devices containing antibodies the separation of CD4 or CD34
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASAH )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine derived
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26-MAY-1998;
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                                                                                                                                                                               illustrate the method of the invention
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DB; AAY51146.
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MEDICAL CO LTD
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98JP-0163023.
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01-APR-1997;
25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemla; myasthenia gravis; multiple sclerosis; Basedow's disease; throughparties and the sclerosis; basedow's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome: Croba'a disease;
                                             New antibodies and proteins bind conserved epitope of Fas antiqued to evaluate drugs in animal models and to treat Fas-associated to evaluate drugs in animal models and to treat Fas-associated to evaluate disease, allergy, atopy, arterioscles
                                                                                                                                                                                                                                                                                                                                                                                                                 thrombopenia purpura: insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; ds.
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15-MAR-1999
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97JP-0082953
97JP-0169088
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myocarditis, hepatitis

and

AIDS

atopy, arteriosclerosis

Reference

Example

4.

Page 188-189;

292pp;

English

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AAA72109
ID AAA7
XX AAA7
AC AAA7
XX 24-1
XX CCDN/
XX Ant
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                                                                                                                             murine; complementarity determining région; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autolmmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophth
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                                                                                                                 cardiomyopathy; hepatitis; AIDS;
                                                                                                                                                                                                                                            cDNA encoding mouse anti-Fas antibody HFE7A light chain.
                                         JP2000169393-A
                                                                              Mus musculus.
                                                                                                                                                                                                         Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828
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94.6%;
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Best Local S
Matches 315
                                                                                                                            AAA11547 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents cONA and organ light chain of the murine anti-human Fas monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fray/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs
                               Murine anti-Fas antibody HFE7A light chain cDNA
                                                               08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-Fas antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 69-70; 139pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preventive or treating agent
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as antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                                                                                      ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA
                                                                                                                                                                                                                                  ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA
                                                                                                                                                                                                                                                                  CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
                                                                                                                                                                                                                                                                                                                             GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                                                                                                                                                                                             GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;
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                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0276883
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                                                                                                                            cDNA;
                                                              entry)
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94.6%;
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Pred. No. 8.5e-81;
0; Mismatches 15;
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murine; anti-inflammatory; anti-anemic;

antidiabetic;

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cc immunomodulatory, dermatological, immunosupersive, thyrometic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, cardinart and hepatropic activity. (1) induce cc apoptosis by binding to cell surface Fas or inhibit it by competitive cc inhibition of ligand binding. (1) are used to treat and/or prevent cd seases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's cc disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, cmultiple sclerosis, Basedow's disease, thrombopenia purpura, insulin cc dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cc cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (8, C or D) or alcoholic), and transplant rejection. (1) selectively cinhibit apoptosis in normal cells but selectively induce it in abnormal cc list the protesis in mormal cells but selectively induce it in abnormal collistication of the active site of Fas, i.e. they mimic the nutrine anti-murine antibody response. This sequence encodes camurine anti-ras monoclonal antibody HFE7A light chain described in the
                                                                                    Matches
                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the state of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, incomposition of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermatological; immunosuppressive; thyromimetic; antirhoumatic; anti-FR nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7/ Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; moodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1998;
30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-258930/23
    61
                                                                                                    Similarity
GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                  GACATTGTGCTCACCAATTCTCCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                                                  714
                                                                                                                                                               BP;
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                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0276881
98JP-0276882
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                                                                                                    88.8%;
94.6%;
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                                                                         Score 293; µb
Pred. No. 8.5e
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                                                                                                                                                             157 T;
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                                                                                                DB 21;
.5e-81;
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                                                                                                                     Length
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GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC

Matches 315; Query Match Best Local

Conservative

0; Score Pred.

Mismatches NO. 8 DΒ

15;

Indels

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Gaps

60

Length 714;

Local Similarity

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RESULT 11
ABL45926
                                    The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antiallergic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others.
Sequence 714 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                              ·P-PSDB; ABB74904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             light chain subunit; apoptosis; immunosuppressive; autoimmune disease; allergy; atopic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse humanised anti-Fas antibody related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2000; 2000JP-0090918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL45926 standard;
                                                                                                                                                                                                                                                                                                                                                containing humanised anti-Fas antibody, used ting autoimmune diseases, allergy, and atopy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-145113/19.
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                                                                                                                                                                                                                                                                                                       (Preparatory); Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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200 A; 184 C; 173 G; 157 T; 0 other;
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                                                                                                                                                                                                                                                                                                    77-79; 194pp; Japanese
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RESULT 12
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AC ABL48
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DW Humar
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Humar
XW heavy
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Query Match
Best Local S
Matches 315
                                                                                  The invention relates to a preventive or treating agent for diseases caused by abnormality in the Fas/Fas ligand system containing, as the active component, an antibody having a light chain subunit and a hactivity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antiallergic, immunosuppressive and apoptotic activity and is used for preventing and treating autoimmune diseases, allergy, atopy are
                                                                                                                                                                                                                         Drug
                                                   Sequence
                                                                                                                                                                                  Example 1; Page 112-114; 154pp; Japanese.
                                                                                                                                                                                                               comprises
                                                                                                                                                                                                                                                   p-pSDB;
                                                                                                                                                                                                                                                                                                               29-MAR-2000; 2000JP-0091144
                                                                                                                                                                                                                                                                                                                                      28-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain; heavy chain; apoptosis; antiallergic; immunosuppressive; apoptot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised anti-Fas antibody heavy chain encoding DNA SEQ ID NO 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-2002
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                                                                                                                                                                                                                                                                                       (SANY ) SANKYO CO LTD
               Local Similarity
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                                                                                                                                                                                                             preventing humanised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    disease; allergy; atopy; gene;
                                                   BP;
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                                                   200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                            or treating e.g. autoimmune anti-Fas antibody
            88.8%;
94.6%;
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                                                C; 173 G; 157 T; 0 other;
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Score 293; DB Pred. No. 8.5e O; Mismatches
           DB 24;
.5e-81;
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                                                         Query Match
Best Local S
Matches 315
                                                                                                                        The invention provides an antibody having affinity to CD4 antigen. anti-human CD4 antibody 4H5 is used for the detection of antigen are application for drugs. It is highly safe in human dose. The present sequence represents the antibody 4H5 H chain encoding nucleotide
                                                                                                                                                                                                                                                                                                                                          Mus
                                                                                               Sequence
                                                                                                                  sequence
                                                                                                                                                                       Disclosure; Page 16-17; 25pp; Japanese.
                                                                                                                                                                                            An antibody
                                                                                                                                                                                                                                                                                                    07-DEC-1999
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les 315; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                         Conservative
                                                                                               В₽;
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Pred. No. 9.3e-81;
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                                                                                             198 T; 0 other;
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Matches 315
                                                                                                                                                                                                   The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the antibody 4H5 L chain encoding nucleotide
                                                                                                                                                                                                                                                              Disclosure; Page 17-18;
                                                                                                                                                                                                                                                                                  An antibody and the nucleic acid coding the
                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-1999
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                                                                                                                                      Similarity
CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                       GACATTGTGCTCACCAATTCTCCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                                                       925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                               ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGATGATAGTTATATATG.---TGGTAC
                                                                             GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 399
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                                                                                                                          Conservative
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                                                                                                                                  88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding nucleotide sequence.
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                                                                                                                                                                                                                                                           25pp; Japanese.
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                                                                                                                       Pred. No. 9.3e
0; Mismatches
                                                                                                                                    Score 293; DB 21;
Pred. No. 9.3e-81;
                                                                                                                                                                      268 G; 198 T; 0 other;
                                                                                                                                                                                                                                                                                    antibody
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Mismatches

Indels

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Gaps

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RESULT 15
AAZ44205
                                                     Query Match
Best Local S
Matches 315
                                                                        This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence encodes a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                      (ASAH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ44205 standard;
                                                                                                                                                                                                                         Claim 22;
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ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL KEYWORDS SOURCE ORGANISM ACCESSION VERSION LOCUS DEFINITION RESULT 1 BF137298 COMMENT cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution infood through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 15 High quality sequence stop: 657. Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Unpublished NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 659) Mus musculus EST mRNA sequence. BF137298 BF137298.1 GI:10976338 BF137298 659 bp mRNA linear EST 24-OCT-2000 601781658F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009670 5', Mus musculus (house mouse) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus Ph.D. information (LLNL) can эd

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                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 407)
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/clone_lib="NCI_CGAP_Lu30"
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Location/Qualifiers
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RNA of mice of the same strain Int. J. Radiat. Biol. Relat. St
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vercenteria;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

1 (bases 1 to 683)

Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H.,

Tlan,F.R., Yan,X.J., Hou,Y. and Su,C.Z.

Mechanism of exogenous nucleic acids and their precursors implementary of intestinal epithelium after gamma-irradiation the repair of intestinal epithelium after gamma-irradiation of the repair of the repa
Cui,D., Zeng,G., Yan,X., Li,X. and Su,C.
Cloning of mouse genes related to repairing of
epithelium of the irradiated mice by treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus MRP9 mRNA, AF240172 AF240172.1 GI:13877293 HTC.
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                                                                                                                           (bases 1 to 683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with
polylinker; 1st strand cDNA was prepared fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1531021"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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86.5%;
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602835202F1 NCI_CGAP_Co24
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              Eukaryota;
Mammalia;
                                    Mus musculus
                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to Cui,D., Zeng,G.
                                                Mus musculus (house mouse)
                                                                           BG969221.1
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                                                                                                                                                                                                                                                                CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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                                                                                                                                                                                                                                                                                                                                       CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
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  (bases 1 to 1108)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAK43734.1"
/db_xref="G1:13877294"
/db_xref="G1:13877294"
/translation="LCGTRFQRIRIRHRRTCGRPFQLQLGPPSERVRNLLTLVTEIHC
RIILLHRIYVEAEICPRPTASKPGRDPGSLLGCSIDEEFGWLSWFLLEPVHKTNANII
NTFAGSAGDGGPLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="intestinal gland cell"
/note="derived from differential display PCR between
irradiated mice with and without RNA injection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intestinal gland cells treated with
/codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="related to the repair of irradiation-damaged
intestinal gland cells treated with RNA"
           Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="MRP9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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Pred. No. 8e-62;
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                                                                                                              Mus musculus
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           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                mRNA sequence.
BF581989
                                                Mus musculus
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High quality sequence stop: 508.
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 774)
                                                                                                                                                                                                                               BF581989
602099444F1 NCI_CGAP_Co24
NTH-MGC http://mgc.nci.nih.gov/
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Email: cgapbs-r@mail.nih.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="PH10B (Tl phage-resistant)"
/lab_host="PH10B (Tl phage-resistant)"
/clone_lib="NCI_CGAP_CO24"
/clone_tib="NCI_CGAP_CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. primer: Oligo dT:
Average insert size 1.6 kb. Constructed by Life
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/strain="FVB/N"
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
1 (bases 1 to 750)
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
                                                                                                                                           BG965050: 750 bp mRN/ 602829112F1 NCI_CGAP_Co24 Mus musculus
                                                                                                                     mRNA sequence.
BG965050
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                                                                              Mus musculus (house mouse)
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http://mgc.nci.nih.gov/.
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/clone_lib="NCI_CGAP_CO24"
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1 Site_2: Sall; Cloned unidirectionally. Primer: Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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/strain="FVB/N"
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 398)
Marra,M., Hillier,L., Allen,M.
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Contact: Robert Strausberg,
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//lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/clone="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI
/note="Organ: colon; Vector: pCMV-SPORT6; Site_
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85.5%;
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Pred. No. 1.7e-61;
0; Mismatches 45
           Allen, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus"
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                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
           Bowles, M.,
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           Dietrich, N.,
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                                                                                                                                                                              Euteleostomi;
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                                                                                                                         Murinae;
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           Dubuque, T
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                                                                                                                                                                                                                                                                 126 ATCTCCTGCAGAGCCAGCGAAAGTGTTGATAATTCTGGCATTAGTTTTTATGAACTGGTTC
                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                  61 ATCTCCTGCAAGGCCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC
                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theising, B., Wylie, T., Lennon, G., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:492708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                             GGGGTCCCTGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCAGCCTCAACATCCAT
                                                                                                                              GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                   CAACAGAAACCAGGACAGGCACCCAAACTCCTCATCTATGCTGCATCCAACAAAAGATCC
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ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                      CCTATGGAGGAGGATGATACTACAATGTATTTCTGTCAGCAAAGTAAGGAGGTTCCTCGG
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/db_xref="taxon:10090"
/clone="IMAGE:832492"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary gland; Vector: pT713D-Pac (Pharmacia)
/ with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host-"DH10B"
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/dev_stage="4 weeks"
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the modified pT7T3 vector.
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipelline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tayami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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Email: cyapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Mammalla; Eutherla; Rodentia; S
1 (bases 1 to 831)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                               Unpublished Contact: Robert Strausberg, Ph.D.
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KEYWORDS
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Best Local S
Matches 289
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                                                                                                                                                                                                                                                                                             ALD498UU 402 bp mRNA linear EST 23-MAR-1999 ve80a03,yl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:832492 5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN); gb:M35669 Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; N
1 (bases 1 to 402)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anal
Tumor Gene Index
                                                                                                        Unpublished
                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                              Mus musculus (house mouse)
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Plate: LLAM11002 row
                   MGI:492708
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/lab_host="PHIOB (TI phage-resistant)"
/lab_host="PHIOB (TI phage-resistant)"
/clone_lib="NCI_CGAP_CO24"
/clone="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/cloned unidirectionally. Primer: Oligo di Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 219 c 197 g 185 t
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/strain="FVB/N"
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Location/Qualifiers
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86.5%;
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Rodentia;
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Sciurognathi;
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Murinae; Mus
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SOURCE
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                                                                                                                  BG148320 327 bp mRNA linear E uu91c06:y1 Soares_mouse_NMGB_bcell Mus musculus cDNA IMAGE:3383818 5' similar to SW:KV3H_MOUSE P01660 IG K Y-III REGION PC 3741/TEPC 111. ; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This read has been verified (found
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                           BG148320
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                                                                 musculus (house
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary_gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="mammary gland"
/dev_stage="4 weeks"
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/clone="IMAGE:832492"
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/strain="C57BL/6J"
               1 to 327)
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                                                                   mouse)
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Pred. No. 2.4e-60;
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Inpublished
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Email: clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 876)
                                                                                                                                                                                      BI107286 876 b
602894285F1 NCI_CGAP_Lu29 Mus
NIH-MGC http://mgc.nci.nih.gov/
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                                                                                               Mus musculus (house
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the Not I and Eco RI sites of the
Library is normalized; constructed
M.Fatima Bonaldo."
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/lab_host="DH10B (phage-resistant)"
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is normalized; constructed by Bento Soares and
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
l (bases 1 to 735)
                                                                                                                     mRNA sequence.
BG967206
BG967206.1 GI:14354843
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Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished Contact: Robert Strausberg, Ph.D.
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602833889F1 NCI_CGAP_Co24
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Plate: LLAM11108 row: i column:
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Location/Qualifiers
                                                                                   Mus musculus (house mouse)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
cound through the I.M.A.G.E. Consortium/LLNL at:
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/note="Organ: lung; Vector: pCMV-SpORT6; Site_1: Sall;
/note="Organ: lung: Vector: pCMV-SpORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo (
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
242 c 192 g 203 t
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/clone="IMAGE:5039325"
/tlssue_type="spontaneous tumor,
/tmm cell origin."
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            Mammalia; Eutheria; Rodentia;
1 (bases 1 to 865)
NIH-MGC http://mag.
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                     Mus musculus
Eukaryota; M
                                                                                                                                                       mRNA sequence.
BI659552
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_bost="DH10B (T1 phage-resistant)"
/lab_bost="DH10B (T1 phage-resistant)"
/clone_lib="NCI_GGAP_CO24"
/clone_Togan: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo do
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Pred. No. 6.7
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                                                                       Craniata; Vertebrata;
                                                                                                                                                                                             musculus cDNA clone
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EST 12-SEP-2 IMAGE: 5348688

Euteleostomi;

Wilson, R. and

Morris,

Dubuque, T.,

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contact the

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                                      uc25e04.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:199038 5' similar to qb:X02484_rnal IG KAPPA CHAIN PRECURSOR V-IV REGION (HUMAN); gb:M35669 Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence. AI120005
                                                                                                                                      AI120005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM11886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
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Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                                                                                                                                      CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATCCTGCAAGGCCAGCCAGAGTATCAGTTATTACGGTAAAAATTATATCAACTGGTTC
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Mam4"
/note="Organ: mammary; Vector: pcWV-SPORT6; Site_1: SalI_
/note="Organ: mammary; Vector: pcWV-SPORT6; Site_1: Oligo dT
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Grov
and Differentiation 7, 3-11 (1996)."
a 238 c 202 g 192 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tumor, gross
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5348688"
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                                                                                                                                                                                                                                                                                                                                    1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lotel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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h quality sequence stop: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NbMMG"
/clone_lib="Soares_mammary yland; Vector: pT7T3D-Pac (Pharmacia /note="Organ: mammary yland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco ) with a modified polylinker; Site_1 Not I - oligo(dT)
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/dev_stage="4 weeks"
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/strain="C57BL/6J"
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Pred. No. 7.3e-60;
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Bento Soares
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Search completed: September 13, 2003, 06:41:26 Job time : 2602 secs

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Result
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
6: /cgn2_6/ptodata/2/
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Gapop 10.0 , Gapext 1.0
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330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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  DB
B
         US-08-483-636-1
US-08-483-632-1
US-08-483-632-1
US-08-491-845-7
US-08-579-378A-13
US-08-137-117D-32
US-08-275-053-16
US-08-275-053-16
US-08-211-980-21
US-08-211-980-17
US-08-111-080-17
US-08-111-080-17
US-08-211-980-17
PCT-US93-07967-17
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US-08-487-200-66
US-08-487-200-66
US-08-487-200-66
US-08-487-200-66
US-08-487-200-66
US-08-487-200-66
US-08-653-497A-17
US-08-656-906-24
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Sequence 7, Appli
Sequence 7, Appli
Sequence 13, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 10, Appl
Sequence 16, Appl
Sequence
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           17, Appl
5, Appli
66, Appl
67, Appl
67, Appl
68, Appl
69, Appl
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21, Appl
21, Appl
21, Appl
39, Appl
317, Appl
317, Appl
317, Appl
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
229	230.6	231.4	232.2	233.8	233.8	235.4	235.4	237	237	238.6	239.4	242.4	243.4	243.4	243.4	243.4	243.4
69.4	69.9	70.1	70.4	70.8	70.8	71.3	71.3	71.8	71.8	72.3	72.5	73.5	73.8	73.8	73.8	73.8	73.8
396	393	332	654	723	334	428	399	394	394	336	333	783	1797	1797	393	393	333
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Sequence 15, Appl	Sequence 17, Appl	Sequence 58, Appl	Sequence 1, Appli	Sequence 56, Appl		Sequence 4, Appli	Sequence 52, Appl	Sequence 24, Appl	Sequence 24, Appl	Sequence 14, Appl	Sequence 3, Appli	Sequence 19, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 24, Appl	Sequence 24, Appl	Sequence 3, Appli

ALIGNMENTS

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US-08-483-636-1
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GENERAL INFORMATION:
                                TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
                                                                                                                                                        APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant II4 Antibodies Useful TITLE OF INVENTION: Treatment of II4 Mediated Disorder NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Box 1539
CITY: King of Prussia
STATE: PA
                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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SYSTEM: PC-DOS/MS-DOS
unknown
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O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08483632 Patent No. 5928904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Signatches 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483.632
FILING DATE:
CLASSIFICATION:
                          APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10
                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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              07-SEP-199
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94.9%;
                            PCT/US/94/10308
                                                                                                                              US 08/117366
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Pred. No. 3.2e-91;
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                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: MAEDA, Hiroaki
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: EDA, Yasuyuki
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                      STREET:
CITY: Wa
STATE: C
                                                                                                                                         ADDRESSEE: Browdy and Neimark STREET: 419 Seventh Street N.
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Washington : D.C.

Z.V

Ste.

, Application US/08491845 5773247

20004

PatentIn Release #1.0,

Version #1.30

USA

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NAME: Sutton, Jeil...

REGISTRATION NUMBER: 34,000
REFERENCE/DOCKET NUMBER: P5018/
REFERENCE/DOCKET NUMBER: P5018/
REFERENCE/CAPTON INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 270-5024
ITELEPHONE: (215) 270-5024
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                           US-08-483-632-1
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                        Matches 316;
                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..396
                                                                                                                                                     361
                                                      301
                                                                               238
                                                                                                     178
                                                                                                                                                                                                       61 GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                                                                                                                                                              1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
             ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                  CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 393
                                                 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCTCCG
                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                 Score 294.6; DB 2;
Pred No. 3.2e-91;
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                                                                                                                                                                                                                                                                                                                                            Length
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Qy
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; LOCATION:
US-08-491-845-7
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                                                                                                                                                                                                                                                      RESULT 4
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                            Sequence 13, Application US/08579378A Patent No. 6210671 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                             APPLICANT: CO, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactiv
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: One MarketPlaza, Steuart Tower, Suite
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APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MAI
TELECOMMUNICATION INFORMATION:
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                                                                          ADDRESSEE:
STREET: On
CITY: San
                                           STATE: C
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                                 ZIP:
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                                                                          San Francisco
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                                                            California
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(202) 737-3528
                                            USA
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Floppy disk
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                                                                                                                                                             Humanized Antibodies Reactive with
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Pred. No. 1.6e-88;
0; Mismatches 19;
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         US-08-137-117D-32
; Sequence 32, Application
; Patent No. 5795965
; GENERAL INFORMATION:
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APPLICANT:

TSUCHIYA, Masayuki

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US-08-579-378A-13
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Best Local Similarity
Matches 309; Conserv
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FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 951
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 393 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400 TELEFAX: 415-326-2422
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
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361
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                                 ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                    CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 393
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92.8%;
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Pred. No. 2.2e-87;
0; Mismatches 21
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US-08-137-117D-32
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25,258 REFERENCE/DOCKET NUMBER: 53/TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: JP 4-
FILING DATE: 19-FEB-1992
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CITY: Washington
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                181
                                                                                 118 CAACAGAAACCAGGACAGCCACCCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                               121 ATATCCTGCAGAGCCAGTGAAAGTGTTGATAGTTATGGCAATAGTTTTATGCACTGGTAC 180
                                                                                                                                                                                                                                                                296;
                                                                                                                                                61 ATCTCCTGCAAGGCCAAGCCAAAGTGTTGATTATATGATGGTGATAGTTATATG----TGGTAC
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               GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTTCGGGACAGACTTCACCCTCAACATCCAT
                                                             CAGCAGAAACCAGGACAGCCAACCCCAAACTCCTCATCTATCGTGCATCCAACCTAGAATCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
GGGATCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACCCTCACCATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 base pairs
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JONES, Steven
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25-APR-1991
                                                                                                                                                                                                                                                                               79.6%;
88.9%;
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Pred. No. 2.9e-80;
0; Mismatches 34;
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RESULT 6
US-08-436-717-32
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US-08-436-717-32
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:

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MEDIUM TYPE: Floppy disk
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APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                              NAME/KEY:
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20007-5109
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(202)672-5399
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JONES, Steven
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Query Match

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Patent No.
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APPLICATION NUMBER: P
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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95; Conservative
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Pred. No. 9.4e-80;
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            Sequence 21, Application Patent No. 5558865 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: PAPPLICATION OF SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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YPE: nucleic acid

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TOPOLOGY: 1'

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 APPLICANT:
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Local 295;
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Pred. No. 9.4e-80;
Pred. No. 9.4e-80;
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est Local S
Matches 295
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REGISTRATION NUMBER: 25,447
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INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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FEATURE:
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REFERENCE/DOCKET NUMBER: 31629
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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CITY: Chicago
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ADDRESSEE: Borun
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                                                                                       GGGTCCCTGCCAGGTTCAGTGGCAGTCGGTCTAGGACAGACTTCACCCTCACCATTGAT
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ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                              CCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAATAATGAGGATCCGCTC
                                               CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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Pred. No. 9.8e-80;
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US-08-211-980-21
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Best Local :
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FILING DATE: 24 AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REGISTRATION NUMBER: 25,447
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 363 base pairs
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CITY: Chicago
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Pred. No. 9.8e-80;
"" wismatches 35;
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PCT-US93-07967-21
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APPLICATION UNMBER: US 08/039,
APPLICATION UNMBER: US 08/039,
APPLICATION UNMBER: US 08/039,
AFTORNEY/AGENT INFORMATION:
NAME: BOTUN, MICHAEL F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 3169
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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TELEX: 25-3856
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                                                                                  Similarity
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22-APR-1993
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GENERAL INFORMATION:
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                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                  REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: ME
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                  APPLICATION NUMBER: EP 94
FILING DATE: 02-DEC-1994
ATTORNEY_AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33.3
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 9. FILING DATE: 17-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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CITY: A
STATE:
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                   TOPOLOGY:
                                STRANDEDNESS: single
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ROSELL, ELISABET
BLASCO, FRANCESC
PIULATS, JAUME
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                                                                339 base pairs
                                                                                                                    703-243-6410
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ANSELL, KEITH H.
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                   linear
                                                                                                                                       703-243-6333
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17-NOV-1995
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Query Match Best Local S Matches 295

295;

FEATURE:

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RESULT 13
US-08-111-080-17
; Sequence 17, Application 08/111080
. Patent No. 5558865
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Best Local Similarity
Matches 293; Conserv
APPLICATION: 424
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 07/748,562
APPLICATION NUMBER: 1991
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            APPLICANT: Ohno, Tsuneya TITLE OF INVENTION: HIV NUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE: CLONE: L3 11D (light chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: mou
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                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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DEVELOPMENTAL STAGE: adu
TISSUE TYPE: Lymph node
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                                                                                                                                                                                                                                                                                                                            Immunotherapeutics
                                                                                                                     Version #1.25
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RESULT 14
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                                                                                                                                                                                                                                   Sequence 17, Application US/08211980 Patent No. 5665569
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                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Ohno,
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TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                       STREET: Chicago
CITY: Chicago
TTATE: Illinois
                                                                                                                                                           APPLICANT: Ohno, Tsune
TITLE OF INVENTION: HI
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER:
FILING DATE: 22-APR-
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LOCATION:
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                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                   6300 Sears Tower,
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22-APR-1993
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24-AUG-1992
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                                                                                                                                                                                   Tsuneya
N: HIV Immunotherapeutics
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                                                                                                                                              O'Toole,
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Pred. No. 1.:
                                                                                                                   233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                           Gerstein, Murray
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PCT-US92-07111-16
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Best Local S
Matches 293
                                                                                                                          Sequence 16, Application PC/TUS9207111 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOYUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 474-6300
TELECHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
                          APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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TYPE: n
STREET:
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STRANDEDNESS: sing
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SOFTWARE: Patentin Release #1.0, Version #1.25
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           Two First National Plaza, 20 South Clark
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Pred. No. 1.2e-78;
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Best Local.S
Matches 293
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 22-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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STATE: I
COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
PATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
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GCGTTCGGTACTGGGACCAAGCTGGAGCTGAAA
                              ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                               CCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAATAATGAGGATCCGCTC
                                                                               CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
                                                                                                                           GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACCCTCACCATTGAT
                                                                                                                                           GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                     CAGCAGAAACCAGGACAGTCACCCAAACTCCTCATCTATGTTGCATCCAACCTAGAATCT
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IBM PC compatible
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88.0%;
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Pred. No. 1.2
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Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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'Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
'Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
'Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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           1 US-09-759-112A-22

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3 US-10-216-484-51

4 US-10-216-484-108

2 US-10-216-484-108

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           Sequence 22, Appl
Sequence 23, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 3, Appl
Sequence 53, Appl
Sequence 51, Appl
Sequence 108, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 106, Appli
Sequence 17, Appli
Sequence 49, Appl
Sequence 37, Appl
Sequence 43, Appl
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206.6	208	213 208	213	221.6	222.6	222.6	223.8	232.2	232.8	232.8	232.8	237	237.6	237.6	237.6	238.6	238.6	241.8	243.4	243.4	243.4	245	245	246.6	253
58.6 58.4	63.0	63.0	04.51	67.2	67.5	67.5	67.8	70.4	70.5	70.5	70.5	71.8	72.0	72.0			72.3						74.2	74.7	76.7
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US-09-879-461-13 US-09-879-461-57 US-10-244-821-37	-09-782-671B-	US-10-215-484-128 US-09-782-672-1	-10-216-484-	US-10-300-215-89	US-09-742-693-27	US-10-216-484-130	US-09-881-823-13	US-09-917-410-1	-10-150-762-3	-10-013-173-3	-821-	-349-2	-762-4	-173-4	US-10-244-821-46	US-10-160-506-78		-770	-655-	US-10-207-655-253	US-10-207-655-249	US-10-169-351-68	-169	US-09-881-823-1	US-10-171-452A-55
Sequence 13, Appl Sequence 57, Appl Sequence 37, Appl	ر بر <u>د</u>	Sequence 128, Appli	12	e 89,		e 13	13, Āpp	1, Ar	36,	36,	36,	24,	46,	46,	46	78		۲	26	25	24	83	e 67	Sequence 1, Appli	Sequence 55, Appl

ALIGNMENTS

RESULT 1 US-09-759-112A-22

δÃ Q Ъ Дb Qy ; NAME/KEY: gene ; LOCATION: (1)...(330) OTHER INFORMATION: 1F7 VL chain gene US-09-759-112A-22 Sequence 22, Application US/09759112A
Publication No. US20030100741A1
GENERAL INFORMATION:
APPLICANT: Mueller, Sybille
APPLICANT: Kohler, Heinz
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LI
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTI
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22 Query Match Best Local : Matches 330; FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11 LENGTH: 330
TYPE: DNA
ORGANISM: mouse
FEATURE: 121 CAGAAACCAGGACAGCCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCTGGG 61 61 _ 1 GACATTGTGCTCACCAATTCTCCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC Similarity ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATGTGGTACCAA 120 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGTGGTACCAA GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTCTCTAGGGCCAGAGGGCCCACC Conservative 100.0%; 0; Score 330; DB 11; Pred. No. 2.7e-104; Mismatches Length 330; 0 Gaps 180 120 60

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RESULT 3
US-09-879-461-1
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US-09-759-112A-23
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publication No. US20030100741A1
GENERAL INFORMATION:
APPLICANT: Mueller, Sybille
APPLICANT: Kohler, Heinz
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT APPLICATION NUMBER: US/09/759,112A
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LENGTH: 330
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Best Local :
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NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                     CAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCTGGG 180
                                                                                                                                                                                                                                                                                                                                              ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGATGATGATTATATGTGGTGATACCAA 120
                                                                                                                                                                                                                     TTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                                                                         TTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                                                                                                                                                                                                     GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTCTCTAGGGCCAGAGGGCCACC
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ilarity 100.0%;
Conservative (
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Pred. No. 2.7e-104;
; Mismatches 0;
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Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 1..396
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,461

FILING DATE: 12-Jun-2001

CLASSIFICATION: CURROWND

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 -
Swedeland Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/612,929
EILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful introduced Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holmes, Stephen D. Gross, Mitchell S.
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316; Conserv
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                            CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
                                                                     GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
         CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCTCCG
                                                                                                                                                                                                                                   ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC
                                                                                                                                                                                                                                                                 GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19406-2
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STATE: PA
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94.9%;
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Pred. No. 5.7e-92;
D; Mismatches 14;
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ACGTTCGGTGCTGGGACCTAAGCTGGAGCTGAAA 330

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RESULT 5
US-09-903-327A-3
Sequence 3, Application US/09903327A
; Patent No. US20020164333A1
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; LOCATION: (1)..(60)
US-10-216-484-10
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US-10-216-484-10
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APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
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Matches
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APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Hatuyama, Hideyuki
APPLICANT: Nakahara, Kaori
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/10216484 Publication No. US20030103976A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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EQ ID NO 10
LENGTH: 714
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NAME/KEY: CDS
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Similarity 94.6%;
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Pred. No. 2
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.6e-91;
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US-10-216-484-53
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NUMBER OF SEQ I
SEQ ID NO 53
LENGTH: 768
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                                                                                                                                                                                                                                                                                                                              Sequence 53, Ap
Publication No.
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Best Local Similarity
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APPLICANT: Li, Erguang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
CORMMANDE. DESCRED FOR WINDOWS VARSION 4.0
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                                                    CURRENT APPLICATION NUMBER: US/10/216,40 CURRENT FILING DATE: 2002-08-09 PRIOR APPLICATION NUMBER: US/09/499,662 PRIOR FILING DATE: 2000-02-09 PRIOR APPLICATION NUMBER: US 09/053,583 PRIOR FILING DATE: 1998-04-01
                                                                                                                                                                      APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki Ikuko
APPLICANT: Tamaki Ikuko
TITLE OF INVENTION: Anth-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (13)...(726)
OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mouse
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   373
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                                                                                                                                                                                                                                                                                                                                                Application US/10216484
                                        ID NOS:
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93.4%;
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Pred. No. 4.7e-89;
0; Mismatches 19
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PRIOR APPLICATION NUMBER: US/09/49,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 51
LENGTH: 768
TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-216-484-51
Sequence 51, Application US/10216484
Sublication No. US20030103976A1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Anti-Fas Antibodies FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                      NERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
 FEATURE:
                                                                                                                                                                                                                                                                                                                   APPLICANT:
                           FEATURE:
NAME/KEY: CDS
LOCATION: (40)...(753)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Designed DNA OTHER INFORMATION: encoding the light chain of humanized anti-human OTHER INFORMATION: Fas antibody
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Local Similarity 91.3%;
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mat peptide
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Takahashi, Tohru
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Nakahara, Kaori
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                                                                                                                                                                                                                    SEQ ID NO 108
LENGTH: 768
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Best Local
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILLING DATE: 2002-08-09
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DAYE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DAYE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
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Nakahara, Kaori
Tamaki, Ikuko
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                                sig peptide (40)..(99)
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No. 4.6
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1.6e-84;
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US-10-053-530-8
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                                                            US-10-053-530-8
  Best Loc
Matches
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                               Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hayden-Ledbetter, Martha TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins FILE REFERENCE: 390069.401
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/053,530 CURRENT FILING DATE: 2002-01-17 PRIOR APPLICATION NUMBER: US 09/765,208 PRIOR FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ledbetter, Jeffrey APPLICANT: Hayden-Ledbetter,
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0 EQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 38
                                                                     NAME/KEY: V_region
LOCATION: (454)..(825)
OTHER INFORMATION: HEAVY
OTHER INFORMATION: HD37
                                                                                                                            NAME/KEY: misc_feature
LOCATION: (406)..(450)
OTHER INFORMATION: SYNTHETIC
                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (13)..(72)
OTHER INFORMATION: LIGHT-CHAIN LEADER PEPTIDE
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OTHER INFORMATION:
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LOCATION: (73)..(405)
OTHER INFORMATION: LIGHT
OTHER INFORMATION: HD37
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                           OTHER INFORMATION: SYNTHETIC MOUSE
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 Score 272.2; DB 12; Pred. No. 4.7e-84; 0; Mismatches 28;
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Pred. No. 4.6e-84;
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US-10-207-655-8
; Sequence 8, Application US/10207655
; Publication No. US/0030118592A1
; GENERAL INFORMATION:
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                                                                                                                                                                                ; NAME/REY: V.region
; LOCATION: (454)..(825)
; OTHER INFORMATION: HEAVY CHAIN VARIABLE
US-10-207-655-8
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                                                                                                                   Matches
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                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069, 401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ledbetter, APPLICANT: Hayden-Led
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 426
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

FEATURE:

NAME/KEY: misc_feature

(13)..(72)
                                                                                                                                                                                                                                                                                                                              LOCATION: (73)..(405)
OTHER INFORMATION: LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 825
TYPE: DNA
                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                               OTHER INFORMATION: SYNTHETIC
                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (406)..(450)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: SYNTHETIC MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                Similarity
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(73)..(405)
ATCTCCTGCAAGGCCAAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC
                                                                   GACATTGTGCTCACCAATTCTCCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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                                                  GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCCAGAGGGCCACC
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                                                                                                                 Conservative
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Herry A.

Martha (
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90.7%;
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                                                                                                               Score 272.2; DB 1
Pred. No. 4.7e-84;
0; Mismatches 28
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                                                                                                                                                                                               DOMAIN FOR MOUSE ANTI-HUMAN
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APPLICANT: Fett, James W
TITLE OF INVENTION: Chimeric and Humanized And
FILE REFERENCE: 10498/74073
CURRENT APPLICATION NUMBER: US/09/286,240
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 393
                                    RESULT 12
US-10-216-484-106
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; NAME/KEY: CDS
; LOCATION: (1)..(411)
US-09-286-240-1
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       Sequence 106, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 296; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09286240 Patent No. US20020010320A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 39
TYPE: DNA
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       Application US/10216484
5. US20030103976A1
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Mismatches
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RESULT 13
US-10-216-484-49

I Sequence 49, Application US/10216484

Publication No. US20030103976A1

GENERAL INFORMATION:
APPLICANT: Serizawa, No. US2003010397

APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko

APPLICANT: Tamaki, Ikuko
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Best Local S
Matches 292
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LENGTH: 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1988-04-01
NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tamaki, ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Designed DNA OTHER INFORMATION: encoding the light chain of a humanized anti-Fas OTHER INFORMATION: antibody FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: sig peptide LOCATION: (40)..(99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (40)..(753)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                 ACGTTCGGTCAAGGCACCAAGCTGGAAATCAAA
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                                                                                                                                                                                                                                                           CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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87.78;
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Pred. No. 1.7e-78;
0; Mismatches 38
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CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 49
LENGTH: 768
                                                                                                                                                        RESULT 14
US-10-171-452A-37
US-10-171-452A-37
Sequence 37, Application US/10171452A
Debuication No. US20030108518A1
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                                                          GENERAL INFORMATION:
APPLICANT: Frewin, Mark
APPLICANT: Waldmann, Her
APPLICANT: Gorman, Scott
APPLICANT: Hale, Geoff
APPLICANT: RAO, Patricia
APPLICANT: Kornaga, Tade
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Matches
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   APPLICANT:
TITLE OF I
                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Designed DNA OTHER INFORMATION: encoding the light chain of humanized anti-human OTHER INFORMATION: Fas antibody
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NAME/KEY: CDS
LOCATION: (40)..(753)
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INT: Kornaga, Tadeusz
INT: Ringler, Douglas
INT: Cobbold, Stephen
INT: Winsor-Hines, Dawn
INT: WINSOR TRX1 Antibody a
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Gorman, Scott
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Rao, Patricia
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87.48;
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Pred. No. 6e-7
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RESULT 15
US-10-171-452A-43
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APPLICANT: KOTNAGA, Tadeusz
APPLICANT: Ringler, Douglas
APPLICANT: Cobbold, Stephen
APPLICANT: Winsor-Hines, Dawn
TITLE OF INVENTION: TRX1 Antibody and Uses Th
FILE REFERENCE: 6954,58-59
CURRENT APPLICATION NUMBER: US/10/171,452A
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US60/373,471
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US60/345,194
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SEQ ID NO 37
LENGTH: 717
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APPLICANT:
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Best Local Similarity
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APPLICANT: Waldmann, He
APPLICANT: Gorman, Scot
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PRIOR FILING DATE: 2002-10-19
PRIOR APPLICATION NUMBER: GB0122724.8
PRIOR EILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: GB0114517.6
PRIOR FILING DATE: 2001-06-14
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PRIOR TILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR FILING DATE: 2002-04-18
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ORGANISM: Artificial
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; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 43
; LENGTH: 717
; TYPE: DNA
; PRIOR ARTIficial
; FEATURE:
; OTHER INFORMATION: DNA encoding light chain of humanized antibody
US-10-171-452A-43
Search completed: September 13, 2003, 07:50:43 Job time: 223 secs
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                                        118 CAACAGAAACCAGGACAGCCACACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 285 283.4 283.4 283.4 283.4 283.4 283.8 280.8 280.8 277.6 277.6 275.4 275.4 275.4 Score Query Match 700000000000000000 Length DΒ 10000000000 10 10 10 10 10 10 10 10 0 AF112403 0 AF321952 0 MUSIGKAAW AR144017 0 MMU012372 0 MUSIGKAF 108223 AX392999 MUSIGKABBC MUSIGL5B S42888 MMA005355 MUSL34IGKV AR014069 E30617 MUSL71IGKV MUSL93IGKV AF045518 MUSIGKABBH MMVL1E10 MUSIGKABBD MMIGLC413 BD090559 BD090668 E40022 E40830 E02169 MMIGLC310 E40005 E40813 E43359 E31225 E30616 MMIGLC404 S50265 AF207705 E07408 MUSL202IGK BD090542 E30643 IJ AF402256 AY173024 E43359 Humanized a E3125 Device for E30616 Antibody an E30617 Mouse hybri AF045518 Mus muscu M97871 Mouse hybri AR014069 Sequence E354207 V kappa 21AX39299 Sequence E354207 V kappa 21AX39299 Sequence E354207 V kappa E02169 DNA encodin X65092 M.musculus X65092 M.musculus X65092 M.musculus X65092 Mus muscu AF121403 Mus muscu AF121403 Mus muscu AF121403 Mus muscu AF1214017 Sequence AJ012372 Mus muscu AF1174017 Sequence AJ012372 Mus muscu M61046 Mus musculus M61046 Mouse Ig ka X65093 M.musculus B0090559 Drug cont E400250 Drug cont E40020 Drug cont E40030 Humanized a E43376 Humanized E40005 Drug contai E40813 Humanized a E43359 Humanized a E31225 Device for BD090542 Drug cont BD090651 Drug cont E40005 Drug contai E30643 Antibody Description M97869 Mouse hybr:

ALIGNMENTS

AUTHORS TITLE JOURNAL	REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	RESULT 1 E30643 LOCUS
Mitsuharu,O., Takayuki,K. and Ikuo,M. Antibody and nucleic acid encoding the same Patent: JP 1999332563-A 30 07-DEC-1999;	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 333)	Mus sp.	E30643.1 GI:13017209 JP 1999332563-A/30.	Antibody and nucleic acid encoding the same. E30643	E30643 333 bp DNA linear PAT 18-JUN-2001

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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 363)
Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C. Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence unpublished (1992)
Original source text: Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         processed gene.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                             M97869.1 GI:198667
V-region; immunoglobulin light chain; immunoglobulin-kappa
                                                                                                                                                                                                               Mouse hybridoma
                                                                                                                                                                                                                               MUSL202IGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCACC
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                                                                                                                                                                                                                                                                                                                                                            CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                      GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAACAGAAACCAGGACAGCCAACCCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITSUHARU ONO,TAKAYUKI KUSAKA,IKUO MORIMOTO
C12N15/02,A61K39/395,A61K39/395,C07K16/28,C12N15/09,C12P21/08,C12N15/00,
C12N15/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp. (mouse)
JP 1999332563-A/30
07-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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1. .333
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
86 c 84 g
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94.6%;
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1. .333
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Pred. No. 1.1e-88;
D; Mismatches 15
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                                                                                                                                                                                                               kappa-chain
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                                                                                                                                                                                                                           mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 333;
                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                          linear ROD 2
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AUTHORS
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SOURCE
ORGANISM
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BD090542
LOCUS
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VERSION
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Best Local
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                                                                      SANKYO CO LTD
OS MUS muscul
PN JP 2001344
PD 11-DEC-200
PF 28-MAR-200
PI NOBUFUSA S
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JP 2001342148-A/2.
                                                                                                                                                                                                                                                                      714 bp
Drug containing humanized anti-Fas
BD090542
                                                             TAMAKI
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                                                                                                                                                                                                                                                                                                                                                              ACGTTCGGAGGGGGGGCCAAGCTGGAGATAAAA
                                                                                                           Mus musculus (mouse)
JP 2001342148-A/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                 11-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="IgK"
(1.11). .363
/gene="IgK"
/standard_name="L202; m
specificity)"
a 96 c 92 g
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/strain="BALB/c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="SP20-BALB/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sub_species="domesticus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.8%;
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Mus musculus (house mouse)
Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; I
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
I (bases 1 to 714)
Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
Drug containing humanized anti-Fas antibody
Patent: JP 2001342148-A 2 11-DEC-2001;
PC A61K39/395,A61K38/00,A61P1/16,A61P7/06,A61P9/00,A61P9/10, PC A61P13/12,
PC A61P13/02,A61P29/00,A61P37/00,A61P37/06,A61P37/08,A61P43/00//PC C12N15/09,
PC A61K37/02,C12N15/00
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                                                                                                                                28-MAR-2001 JP 2001093106
NOBUFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO
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nes 15;
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Gaps

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297 300 237 240

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 714)

Takahashi, W., Haruyama, H. and Serizawa, N.

Drug containing humanized anti-Fas antibody
Patent: JP 2001342149-A 2 11-DEC-2001;
SANKYO CO LTD

OS Mus musculus (mouse)
PN JP 2001342149-A/2
PD 11-DEC-2001
PF 28-MAR-2001 JP 2001093243
PF 28-MAR-3001 JP 2001093243
PF 28-M
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Drug containing humanized
BD090651 BD090651.1 GI:22636261
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sig_peptide
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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94.6%;
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(61). .(714)
(1). .(60).
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Pred. No. 1.2e-88;
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ORIGIN
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                                                                                                                                                                                                                                  SANKYO CO LTD
OS Mus muscull
PN JP 2000169
PD 20-JUN-200
PF 30-SEP-199
PR NOBUKI SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drug containing anti-F: E40005
E40005.1 GI:18627121
JP 2000169393-A/2.
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                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 714)
Serizawa,N., Haruyama,H., Takahashi,W., Yoshida,H., 1 Okuma,J., Otsuki,M., Shiraishi,A. and Yonehara,S. Drug containing anti-Fas antibody Patent; JP 2000169393-A 2 20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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PI KIMIHISA ICHIKAWA, JUN OKUMA, MASAHIKO
     PART C P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                SHIN YONEHARA
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                                     CDS
                                                                                                                                                                                                                                                                    Mus musculus (mouse)
JP 2000169393-A/2
20-JUN-2000
30-SEP-1999 JP 1999278301
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 mat_peptide
sig_peptide
                                                                                         C07K16/28, C12N5/00, C12N15/00, C12N15/00
                                                                                                                            A61P13/12, A61P31/18, A61P37/06, C12N5/10, C12N15/02, C12N15/09,
                                                                                                                                                              A61K39/395,A61K39/395,A61K39/00,A61P1/16,A61P7/06,A61P9/00,
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
184 c 173 g 15
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1. .714
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94.6%;
 Location/Qualifiers
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(61). (714)
(1). (60).
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Ichikawa, K.,

SHIRAISHI, ΡI

PC PC ΡI Enteleostomi;

Murinae;

PAT 31-JAN-2002

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Best Local
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                                                              source
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                                                                                                                                                                                                                      SM Mus muscullus (house mouse)

SM Mus muscullus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTTGTAATGAGGATCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ATCTCCTGCAAGGCCAAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC
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                                                                                                          3332C
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                                                                           mat_peptide (61). . (sig_peptide (1). . () Location/Qualifiers
                                                                                                                                                 CDS
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                                                                                                                                                                                                                                 NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKUKO TAMAKI C12N15/09, A61K39/00, A61K39/395, A61K39/395, A61P37/02, A61P43/00, C07K16/18, C07K16/18, C12N15/00, C12N1/21, C12N15/10, C12P21/08//(C12N1/21, C12R1:19), C12N15/00, PC
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
184 c 173 g 15
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1. .714
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                                                                                                 Location/Qualifiers
(1). (714)
(61). (714)
(1). (60).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 2E 1 (bases 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 (bases 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 (bases 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Rodentia; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Rodentia; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714)

Examalia; Rodentia; Rodentia; Sciurognathi; Muridae; Mus. 2E 1 to 714

Examalia; Rodentia; Rode
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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ON Device for separating CD4-positive cells and separation results in the cells in the cel
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                                                     GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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                                   GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGGCCACC
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
/db_219 c 255 g 1
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Pred. No. 1.2e-88;
0; Mismatches 15
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Best Local :
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Mitsuharu,O., Takayuki,K. and Ikuo,M.
Antibody and nucleic acid encoding the
Patent: JP 1999332563-A 3 07-DEC-1999;
ASAHI CHEM IND CO LTD
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08,
C12N15/00,
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JP 1999332563-A/3
07-DEC-1999
26-MAY-1998 JP 1998163034
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

El (bases 1 to 925)

RS Mitsuharu,O., Takayuki,K. and Ikuo,M.
Antibody and nucleic acid encoding the same
AL Patent: JP 1999332563-A 4 07-DEC-1999;
ASAHI CHEM IND CO LTD

OS Mus sp. (mouse)
PN JP 1999332563-A/4
PD 07-DEC-1999
PF 26-MAY-1998 JP 1998163034
PF 26-MAY-1998 JP 1998163034
PF 26-MAY-1998 JP 1998163034
PG C12N15/00, TAKAYUKI KUSAKA,IKUO MORIMOTO
PC C12N15/00, CC C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key

Location/Qualifiers
FT source

//cganism='Mus sp. (mouse)'.
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Antibody and nucleic acid e
E30617 GI:13017183
JP 1999332563-A/4.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
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766 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 798
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Lohman, K. L., Buck, D. W., Carrillo, M. A. and Kennedy, R.C.
Characterization of murine monoclonal anti-CD4: epitope recognition, idiotope expression, and variable gene sequence unpublished (1992)
Original source text: Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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               ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA
                                                               CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATACGGATCCTCCC
                                                                                 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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/mol_type="mRNA"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="IgK"
/standard_name="L71;
specificity)"
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nRNA V-region, partial
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RESULT 13
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 AF045518
Mus musculus
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Lohman, K.L., Buck, D.W., Carrillo, M.A.
Characterization of murine monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recognition, idiotope expression, and Unpublished (1992)
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363 bp mRNA linear ROD;
Mouse hybridoma Ig rearranged kappa-chain mRNA V-region,
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Original source text: Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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1.363
1.363
/gene="IgK"
/standard_name="L93; m/
specificity)"
specificity)"
97 c 89 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="SP20-BALB/c fusion
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393 bp mRNA linear ROD 28-FEB-: 5G6 monoclonal antibody kappa light chain variable
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94.0%;
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Pred. No. 1.4e-87;
0; Mismatches 17;
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anti-CD4; epitope
variable gene sequence
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; Murinae; Mus
            ROD 28-FEB-1998
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TITLE
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Local Similarity
298 ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-FEB-1998) Biochemistry, Tufts Universi-
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Connor, K.C., Fa
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region, (IgK) mRNA, partial AF045518
AF045518.1 GI:2906119
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                                                     CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCGTGG
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358. .>393
./gene="IgK"
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61. .357
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1. .>393
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ASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPV
EEEDAATYYCQQSNEDPWTFGGGTKLEIK"
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/product="monoclonal antibody kappa
/protein_id="AAC04546.1"
/db_xref="GI:2906120"
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/mol_type="mRNA"
/strain="C57BL/6"
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94.0%;
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Maeda, H., Kurumi, K., Eda, Y., Shiosaki, K., Nagatomi, K RECOMBINANT ANTI-HIV ANTIBODY AND ITS PREPARATION Patent; JP 1994125783-A 4 10-MAY-1994;
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hypothetical: No;
anti-sense: No;
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28-DEC-1991 JP 1991359808
MAEDA HIROAKI, KURUMI KAZUHIKO, EDA YASUYUK
HI, PI NAGATOMI KIYOSHI, TOKIYOSHI YUKIO
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JP 1994125783-A/4
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/mol_type="genomic RNA"
/db_xref="taxon:10095"
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Synthetic peptides designed from the variable regions of an anti-CDR3 like monoclonal antibody bind to CD4 and inhibit HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-APR-1998) Chardes T., 9921, 15 Avenue Charles Flahault -
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Synthetic peptides derived from the variable regions of an anti-CD4 monoclonal antibody bind to CD4 and inhibit HIV-1 promoter activation in virus-infected cells

J. Biol. Chem. 274 (6), 3789-3796 (1999)
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Mus musculus
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immunoglobulin; light chain;
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GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                  CAACAGAAACCAGGACAGCCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                                     ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC
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/cell_line="F142-63/ST40"
/cell_type="hybridoma"
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/mol_type="mRNA"
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85 c 86 g
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/note="anti-CD4"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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93.7%;
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Search Job tir		В	Qy	В	Qy
Search completed: September 13, 2003, 05:57:54 Job time : 2867 secs		301 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 333	298 ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330	241 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCGTGG 300	238 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297

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Result
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-483-632-73
US-08-437-117D-3
US-08-436-717-33
US-08-621-751A-14
US-08-483-632-58
US-08-483-632-58
US-08-483-632-2
US-08-483-632-2
US-08-485-380-4
US-08-486-397-4
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29.180 Million cell updates/sec
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Sequence
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US-08-326-110A-36	US-08-461-965-7	US-08-486-399-7	US-08-486-397-7	US-08-480-478-36	US-08-465-380-7	US-09-249-473-40	US-09-249-473-4	US-09-249-448-40	US-09-249-448-4	US-09-249-461-40	US-09-249-461-4 ·	US-08-809-455-40	US-08-809-455-4	US-09-249-451-40	· US-09-249-451-4	US-09-249-472-40	US-09-249-472-4
Sequence 36, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 36, Appl	Sequence 7, Appli	Sequence 40, Appl	Sequence 4, Appli										

ALIGNMENTS

RESULT 1 US-08-984-277-7

Sequence 7. Patent No.

7, Application US/08984277 o. 6057421

GENERAL INFORMATION:
APPLICANT: Muller
APPLICANT: Kohler

VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE MONOCLONAL ANTIBODY 1F7

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Query Match
Best Local Similarity
Thes 9; Conserve
                                                                              ; ANTI-SENSE: NO
US-08-984-277-7
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,277
FILING DATE: 3-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-756-8600
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Bucca, Daniel
REGISTRATION NUMBER: 42,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Muller, Sybille APPLICANT: Kohler, Heinz TITLE OF INVENTION: VARIABLE TITLE OF INVENTION: MONOCLE MUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER KEADABLE FORM: .. MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                Conservative
                               100.0%;
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                               Score 54; DB 3; Pred. No. 0.0072;
                Mismatches
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                                             Length 28;
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               Gaps
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US-08-483-636-20

Application US/08483636

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US-08-483-632-20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                    GENERAL INFORMATION:
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                                                                      tent No.
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (215) 270-509
NFORWATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10:
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: CREECE 196FERN
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Holmes, Stephen D. APPLICANT: Gross, Mitchell S.
   PPLICANT:
                     PLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.U. DU.
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sutton, Jeffrey A.
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STREET: P.O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
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                                                                                    Application US/08483632
                                                                                                                                                                                                                                                                                                                                                                                       9 amino acids
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Holmes, Stephen D. Gross, Mitchell S. Sylvester, Daniel R.
                                                                                                                                                                                                                                              Conservative
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77.8%;
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Pred. No. 2.5e+05;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                            Length 9;
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                                                                                                                                                                                                  ; Patent No. 5914110
; GENERAL INFORMATION:
APPLICANT: Holmes, S
APPLICANT: Gross, Mi
APPLICANT: Sylvester
                                                                                                                                                                                                                                                                                                                   US-08-483-636-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-483-632-20
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Sequence 73, App. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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PRIOR APPLICATION DATA:
APPLICATION UNWBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (215) 270-50 INFORMATION FOR SEQ ID NO:
                                                                                                                          APPLICANT: Sylvester, D. TITLE OF INVENTION: Rec. TITLE OF INVENTION: Tre. NUMBER OF SEQUENCES: 75 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 270-5024
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APPLICATION NUMBER: US 08/117366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.U. TOTTY: King of Prussia
                                                                    ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220
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                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19406-0939
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COUNTRY: USA
ZIP: 19406-0939
                                                    CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                             Application US/08483636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 amino acids
                                                                                                                                                                                                    Holmes, Stephen D. Gross, Mitchell S. Sylvester, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
                                                                                                                                                                 Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-483-632-73
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Best Local S
Matches 7
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TELEPHONE: (215) 270-5024
TELEPAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
FILING LALL.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
APPLICATION NUMBER: 07-SEP-1993
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYDE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant
TITLE OF INVENTION: Treatment o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Holmes, Stephen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-OCT-1993
NIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US .0 PILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                     ITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
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Pred. No.
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RESULT 6
US-08-137-117D-33
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Best Local Similarity
                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: WO PCT
FILING DATE: 24-APR-1992
PRIOR APPLICATION UMBER: UP 4-3
APPLICATION UMBER: UP 4-3
FILING DATE: 19-FEB-1992
PRIOR APPLICATION UMBER: UP 3-9
PRIOR APPLICATION UMBER: UP 3-9
FILING DATE: 25-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (215) 270-509
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 14 -OCT-11:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO
                                                                                                                                                                                                                          ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: 'Sutton, Jeffrey A.
                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: RESHAPED HUMAN TITLE OF INVENTION: INTERLEUKIN-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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                 WEGNER, Harold C.
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                                                                                                                                                                                                                                                                                                                                                                                                                             E: Foley & Lardner 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SALDANHA, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BENDIG, Mary
JONES, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Masayuki
                                                                                                                              JP 4-32084
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                                                                              JP 3-95476
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             25,258
53466/126/AAOK
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 500
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 Ami-
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                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 3-95476
FILING DATE: 19-APR-1991
PRIOR APPLICATION NUMBER: UP 3-95476
PRIOR APPLICATION NUMBER: UP 3-95476
PRIOR APPLICATION NUMBER: UP 3-95476
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                          NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR NUMBER OF SEQUENCES: 158
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LENGTH: 131 amino acid
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                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Foley & I
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Local Similarity 77.8%;
nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
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TOPOLOGY: linear
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5817790
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3000 K Street, N.W., Suite 500
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JONES, Steven
SALDANHA, JOSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSUCHIYA, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/436,717
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RESULT 9
US-08-621-751A-14
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US-08-621-751A-10
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                                                                                                                                                                                                                           US-08-621-751A-10
                                                                                                                                                            Query Match .
Best Local Similarity
Matches 7; Conserv
Sequence 14, Application US/08621751A Patent No. 5882644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
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APPLICANT: Chang, Chung N.
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Marcin, Ulrich
                                                                                                                                                                                                                                                                                                                    TELEX: 706141 MRSN FOERS SFO INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                         TOPOLOGY: li
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acid
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lebnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
ODERATING SYSTEM: .PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,751A
FILING DATE: 22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON
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les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                               113 QQSNEDPPT 121
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                                                                                                                                                                                                                                                                                      131 amino acids
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                                                                                                                                                                                                                                                                                                                                                      (650) 494-0792
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                                                                                                                                                               Conservative
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MONOCLONAL ANTIBODIES SPECIFIC FOR THE PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND METHODS OF USE THEREOF
                                                                                                                                                                            70.4%: Score 38; 77.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    321152000100
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                            DB
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                           ۵.
                                                                                                                                                                                          Length 131;
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                                                                                                                                                               Gaps
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GENERAL INFORMATION: APPLICANT: Chang,

APPLICANT:

Chang, Chung N. Landolfi, Nicholas F.

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Query Match
Best Local Similarity
""" hes 7; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,751
                                                                                                                                                                                                                                                                                                                                                                                                                      SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 70614 MRSN FOERS SFO
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Martin, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                               APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful ir
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
TUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           quence 58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-483-636-58
                                                                 ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTWADE: Batchtin Bolaco #10
                                                                                                                                                                                                                                                                                                                                                                                                                                        ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 321
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON
                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 755 PAGE CITY: PALO ALTO
                                                                                                                                                                                                                            ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2
CLASSIFICATION:
FILING DATE:
                                                                                                                                                                                                      CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 131 amino acids
amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08483636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.48;
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METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                         Recombinant IL4 Antibodies Useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.30
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               US/08/483,636
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 11
US-08-483-632-58
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Patent No. 5928904
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                                  APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
APPLICATION NUMBER: PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (215) 270-5090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 01
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 07-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 QQSNEDPPT 120
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                                        PCT/US/94/10308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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US-08-483-632-58
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Best Local Similarity
Conserva
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                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                          TELEFAX: (215) 270-50
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-483-636-2
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INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                      NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gross, Mitchell S. APPLICANT: Sylvester, Daniel TITLE OF INVENTION: Recombina TITLE OF INVENTION: Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. Box 1939
CITY: King of Prussia
                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/483,636 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
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                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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TYPE: protein
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                                                   132 amino acids
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P.O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sylvester, Daniel R.
IVENTION: Recombinant IL4 Antibodies Useful in
IVENTION: Treatment of IL4 Mediated Disorders
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77.8%;
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Pred. No. 16;
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                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-483-632-2'
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:

PRIOR APPLICATION NUMBER: US 08/117366

APPLICATION NUMBER: US 08/117366

FILLING DATE: 07-SEP-1993

PRIOR APPLICATION NUMBER: US 08/136783

PRIOR APPLICATION NUMBER: 1930

PRIOR APPLICATION NUMBER: PCT/US/94/10308

APPLICATION NUMBER: PCT/US/94/10308

APPLICATION NUMBER: 07-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: SULTON, Jeffrey A.

REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Holmes
                                                                                                                                                                                                                              TELEFAX: (215) 270-5090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/483,632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220
                                                                                                                                                                                                              LENGTH:
113 QQSNEDPPT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 QQSNEDPPT 121
                                 1 QLCNEDPPT 9
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77.8%;
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77.8%;
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                                                                                   Score 38; DB
Pred. No. 16;
                                                                      Mismatches
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RESULT 14 US-08-465-380-4

Patent No. GENERAL II

INFORMATION:

4

Application US/08465380

APPLICANT:

George P. Vlasuk, Patric H. Stanssens, Joris H.L. Mensens, Marc J. Lauwereys, Yves R. Larcohe, Laurent S. Jespers, Yannick G.J. Gansemans, Matthew Moyle,

APPLICANT:

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                                                                                                                                                                                        RESULT 15
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                          Sequence 40,
                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Peter W.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08 FILING DATE: June 5, 1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON OPERATING SYSTEM: SOFTWARE: WORD PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Ancyclostoma caninum
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                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                          Application US/08465380
                                                                  George P. Vlasuk, Patric H. Stanssens, Joris H.L. Mensens, Marc J. Lauwereys, Yves R. Laroche, Laurent S. Jespers, Yannick G.J. Gansemans, Matthew Moyle,
                                                        Peter W. Bergum
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ADDRESS:
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21;
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Search completed: September 10, 2003, 17:43:23 Job time : 14.05 secs
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: Ancyclostor
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: IBM P.C.
SOFTWARE: WOO'D POFFECT 5.1
CURRENT APPLICATION NUMBER: US/08/
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBET 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                              Local Similarity nes 5; Conserv
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STATE: California
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STREET: Suite 4700
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83.3%;
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    Mismatches

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Pred. No. 21;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                Score
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seq length: 2000000000
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Match Length DB
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/ cgn2_6/ptodata/2/pubpaa/USG_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USG_PUBCOMB.pep:*
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/ cgn2_6/ptodata/2/pubpaa/USGB_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USGB_NEW_PUB.pep:*
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US-09-879-461-20
US-09-879-461-80
US-09-879-461-58
US-09-879-461-2
US-09-498-272-4
US-09-498-272-40
US-09-498-272-7
US-09-498-272-7
US-09-498-272-7
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US-09-759-112A-24
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  Sequence 36, Appl
Sequence 27, Appl
Sequence 26, Appl
Sequence 20, Appl
Sequence 80, Appl
Sequence 80, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 4, Appl
Sequence 40, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 3695, Ap
Sequence 3695, Ap
                                                                                                                                                                                                                                                                                                                                       Description
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RESULT 1 US-09-759-112A-36

Sequence 36, Application US/09759112A Publication No. US20030100741A1 GENERAL INFORMATION:

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	666666666666666666666666666666666666666	4.4
	144 176 176 177 173 177 177 177 177 177 177 177 177	356
	11551542; 155155454545454545454545454545454545454	12
ALIGNMENTS	\$\(\color{1}\) \(\color{1}\) \	10-017-161 09-718-626
	equence 3, Applequence 3, Applequence 3, Applequence 3, Applequence 3, Applequence 34, Applequence 34, Applequence 34, Applequence 34, Applequence 689, Applequence 684, Applequence 684, Applequence 686, Applequ	v ⊢ v

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RESULT 2
US-09-759-112A-24
; Sequence 24, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heiner
                                                                                                                                                                                                                                             á
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Thes 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mueller, Sybille
APPLICANT: Mueller, Sybille
APPLICANT: Mueller, Sybille
APPLICANT: Mueller, Sybille
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 9
TYPE: PRT
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: mouse
                                                                                                                                                                                                                                1 QLCNEDPPT
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0;
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Pred. No. 4.8e+05;
D; Mismatches 0;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-10-085-2108-26
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Best Local Similarity
Thes 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SOFTWARE: PatentIn version 3.0; SEQ ID NO 24; LENGTH: 110; TYPE: PRT; ORGANISM: mouse US-09-759-112A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-085-108-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application us/100, Publication No. US20020178865A1 PUBLICAL INFORMATION: APPLICANT: LUCAS, Sophie TITLE OF INVENTION: COST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: OF MONOCLONAL ANTIBODY
TITLE OF INVENTION: ANTIBODIES
FILE, REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
                                                                                                                          TELEFAX: (212) 318-3400 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 APPLICATION NUMBER: 09/501,104
FILING DATE: 09-Feb-2000
APPLICATION NUMBER: 09/468,433
FILING DATE: December 17, 1999
APPLICATION NUMBER: 09/66,281
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REGISTRATION NUMBER: LUD 5611.1 JEL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/085,108
FILING DATE: 01-Mar-2002
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 26
CORRESONDENCE ADDRESS;
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 QLCNEDPPT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QLCNEDPPT 9
                                       TYPE: amino acid STRANDEDNESS: single-stranded TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                         LENGTH: 407
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N: ISOLATED NUCLEIC ACID MOLECULES CODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-MAGE-B FAMILIES AND USES THEREOF
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Pred. No. 0.054;
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                                                                                                                                                                                                 Sequence 20, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 94
LENGTH: 399
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Best Local Similarity
Matches 6; Conserv
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Best Local S
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APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3
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                                                                                                 NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     279 MCDDDPPT 286
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5; Conserva
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                                                                  CITY: King of Prussia STATE: PA
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Spaulding, Vikki
Wong, Gordon G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, Hilary
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Treacy, Maurice
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Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09729674
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75.0%; Pred. No.
tive '1; Mismatc
                                                                                                                                                                                   Treatment of IL4
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32;
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                                                                                                                                                                                     Mediated Disorders
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RESULT 7
US-09-879-461-58
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Matches
Sequence 58, Application US/09879461 Publication No. US20020193575A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
URRENT APPLICATION NUMBER: US/09/144,886
URRENT FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: 186 region VL epitope 1
                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                          Local Similarity
ses 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknowns
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P50186-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                          93
                                                                                                                                           1 QLCNEDPPT 9
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                                                                                                          QOSNEDPPT 101
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FILING DATE: 12-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: I
SOFTWARE: Patentin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 270-5024
                                                                                                                                                                              Conservative
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                                                                                                                                                                                            70.4%;
77.8%;
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77.8%;
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                                                                                                                                                                                            Score 38; DB 10;
Pred. No. 29;
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Pred. No. 4.8e+05;
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                                                                                                                                                                                                             Length 112;
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Query Match
Best Local Similarity
Thes 7; Conserve
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                                                                                                                                                                                                                                                                         Sequence 2, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Holmes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION UNMBER: US/09/879,461
FILING DATE: 12-Unn-2001
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION DATA:
ADDITORMENT: ....
                                                                                                                                                                        APPLICANT: Holmes, Stephen D.
Gross, Micchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,0
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKilne Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 -
Swedeland Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, 1
Swedeland Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross, Mitchell S. Sylvester, Daniel R. TITLE OF INVENTION: Recombinant
                                                                                                                                                        NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                       112 QQSNEDPPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QLCNEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215)
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
                                                   CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 131 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 10;
Pred. No. 34;
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Query Match
Best Local Similarity
Marches 5; Conserve
                                                                                      US-09-498-272-4
                                                                                                     RESULT 10
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; ORGANISM: Homo sapiens
US-10-207-655-172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-207-655-172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERRACE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TYPE: amino acid
                              Sequence 4, Application US/09498272 Publication No. US20030113890A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          MUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 172
LENGTH: 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 172, Application No. US200 GENERAL INFORMATION:
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
                                                                                                                                                                                                                                                                                                                                                                                                                                       URRENT APPLICATION NUMBER: US/10/207,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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           ÁPPLICANT: Vlasuk, George Phillip
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                                                                                                                                                               22 ELCDDDPP 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QLCNEDPPT 9
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7; Conserva
                                                                                                                                                                                               1 QLCNEDPP 8
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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o. US20030118592A1
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77.8%;
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                                                                                                                                                                                                                                                       Score 38; DB 15;
Pred. No. 69;
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RESULT 11
US-09-498-272-40
; Sequence 40, Application US/09498272
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US-09-498-272-4
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Best Local S
Matches 5
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 09/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: WOO'D PERfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                             ORGANISM: Ancyclostoma caninum SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                         MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
25 CNEEPP 30
                                         3 CNEDPP 8
                                                                                    Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 90071
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                                                                                      Conservative
                                                                                                                                                                                                                                                                                                         amino acid
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Jespers, Laurent Stephane
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Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gansemans, Yannick Georges Jozef
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                                                                                  66.7%; Score 36; DB 11; Length 77;
83.3%; Pred. No. 44;
live 1; Mismatches 0; Indels
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
                                                                                                                                                                                ORGANISM: Ancyclostoma caninum SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                        MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 216/270 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-Feb-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
25 CNEEPP 30
                                      3 CNEDPP 8
                                                                                                                                                                                                                                                               LENGTH: 77 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C.
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/498,272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BIGGS, SUZANNE L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: Time 5 08/465,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/13231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
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                                                                              Conservative
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Messens, Joris Hilda Lieven
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Moyle, Matthew
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Laroche, Yves Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 4700
                                                                          66.7%; Score 36; DB 11; 83.3%; Pred. No. 44; tive 1; Mismatches C
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                                                                                                                  Length 77,
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UKGANISM: Ancyclostoma caninum;
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-498-272-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-498-272-7
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Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 13, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: IBM P.C. SOFTWARE: WOR'D PERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bergum, Peter w.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5"
                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-Feb-2000 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 633 West Fifth
Suite 4700
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/498,272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 9007:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
                                                                                                                                                                                                               LENGTH: 81 amino acids
                                                                                                                                                                                                                                                                                        TELEFAX:
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  Conservative
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Messens, Joris Hilda Lieven
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            66.7%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette, 1.44 Mb
  1;
                    Score 36; DE
Pred. No. 46;
  Mismatches
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                                  DB 11; Length 81;
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Indels
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Gaps
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3 CNEDPP 8

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ORGANISM: Ancyclostoma caninum sequence DESCRIPTION: SEQ ID NO: 20: US-09-498-272-20
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US-09-498-272-20
    Query Match
Best Local S
Matches 5
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                                                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COLOGY
COMPUTER: IBM COLOGY
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Peb-2000
PRIOR APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/361,965
FILING DATE: OCTOBER: 08/326,110
FILING DATE: OCTOBER: 08/326,110
FILING DATE: OCTOBER: 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
    Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 90071
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
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                        66.7%;
83.3%;
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  Score 36; DB:
Pred. No. 57;
1; Mismatches
                                             11; Length 100;
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                                                       US-10-156-761-7554
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; OTHER INFORMATION:
US-09-764-891-3695
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US-09-764-891-3695
                                                                                                                                                              APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3695, Application US/09764891 Publication No. US20030077808A1
Query Match
Best Local Similarity
                                                                                                                            SEQ ID NO 7554
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7554, Application US/10156761 Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10-156-761-7554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                 NUMBER OF SEQ ID NOS: 15109
                                                                LENGTH: 181
TYPE: PRT
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA,
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NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE LOCATION: (90)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 OMCCETPPT 34
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66.7%;
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                 DB 15;
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Search completed: September 10, 2003, 17:50:28 Job time : 19 secs	Oy 2 LCNEDPPT 9 . Db 67 LCOEGPPT 74	Matches 6; Conservative 0; Mismatches
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Result
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Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                       Score
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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ABG20915
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ABU08934
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AAY91016
Murine Mab 117 lig
Human tumour rejec
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Novel human diagno
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272	272	272	249	247	238	212	211	132	132	132	131	131	131	131	131	131	111	111	60	52	9	9	9	0	0	9	399	9	ø	œ	\vdash	99	78	77		J A
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AAR79389	052	AAP50001	39	4	AAP70375	***	~	AAY18120	AAY23767		2	AAY23779	AAW30278	AAW30274	AAR70202	AAR29008	AAY18123			· ABU56909	AAY18116	AAY23774	AAR70197	ABP75688	ABG03085	ABB55744	AAU39035	867	682	5	ABG18624	ABG25273	398	411	7	C1 0 7 0
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ALIGNMENTS

RESULT 1 AAO18542 ID AAO1

AAO18542 standard; Peptide; 9 AA.

AA018542;

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WPI; 2002-590668/63.
N-PSDB; AAL48667.
                                             Muller S,
                                                                                                                                                                Mus sp.
                                                                                                                                                                                   complementarity determining region; framework-determining region; FR; heavy chain; light chaih; HIV infection.
                                                                                                                                                                                                     Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
                                                                                                                                                                                                                        Murine Mab 1F7 light chain CDR3 region.
                                                                                                                                                                                                                                           11-OCT-2002 (first entry)
                                                                                   11-JAN-2001; 2001US-0759112
                                                                                                      11-JAN-2002; 2002WO-US00927.
                                                                                                                          18-JUL-2002.
                                                                                                                                             WO200255668-A2
                                                                 (IMMP-) IMMPHERON INC.
                                             Kohler H;
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New polynucleotide encoding a complementarity- or framework-determining

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RESULT 2
AAY91016
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                                                 The present invention describes the variable heavy and light chain regions (I) of murine monoclonal antibody (mAB) 1F7. AAY91014 to AAY91016 represent specifically claimed amino acid sequences of the variable light chain, and AAY91017 to AAY91019 represent specifically claimed amino acid sequence of the variable heavy chain. The antibodies are used for treatment of HIV (human immunodeficiency virus) infection and AIDS (acquired immunodeficiency syndrome). They are also used for detecting HIV in serum and for stimulating HIV antiger related and committed B cells to produce broadly reactive and neutralising antibodies by clonotypic stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in vaccines against HIV \, -
                                                                                                                                                                                                                                                                                                        Muller S,
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                                                                                                                                                                                                                                    Variable heavy and light chain regions of murine monoclonal antibody 1F7, useful for treating HIV infection and AIDS -
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                          Sequence
                                                                                                                                                                                                          Claim 1; Fig 8; 45pp; English
                                                                                                                                                                                                                                                                              WPI; 2000-338622/29.
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S; anti-HIV; human immunodeficiency virus; detection;
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Query Match

100.0%;

Score

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Human tumour

rejection antigen

precursor, MAGE-B6

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ABU08934
ID ABUU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
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                                                                                                                           ABU08934;
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                                                                                                                                                                                                                                                                                                     92
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RESULT 5
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24-APR-1998;
17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                               determining presence of cytolytic T-cells specific for complexes of hum leukocyte antigen (HLA) and a peptide derived from the nucleic acid in cytotoxic T-lymphocyte (CTL) containing sample. The nucleic acid is useful as a diagnostic probe to determine the presence of abnormal (tumour) cells such as seminoma, bladder transitional-cell carcinoma, head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma, cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express MAGE-B5 or MAGE-B5. The nucleic acid is useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                   disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPs or tumour rejection antigens (TRAP). The present sequence represents the amino acid sequence of the human rumour processions.
Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder
                                              Novel human diagnostic protein #23963.
                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule which encodes a tumour rejection antigen precursor (TRAP) having an amino acid sequence of a TRAP encoded by a fully defined MAGE-C3, MAGE-B5 polynucleotide sequence. Also disclosed is a method which is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding tumor rejection antigen precursor MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or MAGE-B6 -
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                                                                                 18-FEB-2002
                                                                                                                                               ABG23972 standard;
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                                                                                                                                                                                                                                                                                           Conservative
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98US-0066281.
99US-0468433.
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                                                                                                                                               Protein; 54 AA
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                                                                               entry)
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Pred.
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43;
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                forensic;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (II) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                    ABP09856 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                               24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scification, but was obtained in electronic format
ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                           sequence SEQ ID NO: 19694.
                                                                                                                                                                                                  Protein; 54
                                                                                                                                                                                                                                                                                                                                                                                   72.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                   Score 39;
Pred. No.
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RESULT 7
ABG20915
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                        bone degenerative disorders, or periodontal disease, and for gut
protection or regeneration and treatment of lung or liver fibrosis,
reperfusion injury in various tissues and conditions resulting from
systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                         ABG20915;
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, hamourinage, osteomethitis, neurodegenerative disorders, disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (referred to as open reading frame, ORFX, where X is 1-11491 (see in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID 19694; 1037pp; English
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29-AUG-2000; 2000US-228716P.
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 13-FEB-2002
                                                                         ABG20915 standard; Protein; 70
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                                                                                                                                                                                                                                                                                                                                                                                        specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed
                                                                                                                                                                             39
                                                                                                                                                                                                                                                     Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                54
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(first entry)
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                                                                                                                                                                                                                                                                       72.2%;
66.7%;
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                                                                                                                                                                                                                                                         Mismatches
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RESULT 8
ABG15042
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AC ABG1
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                     ABG15042;
                                                                                                        ABG15042 standard; Protein; 73
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                                                                                                                                                                                                                                                                                                                                      70 AA;
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to isolated polynucleotide (I) and II) sequences (I) is useful as hybridisation probes.
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Pred. No. 18;
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Novel human diagnostic protein #15033.

18-FEB-2002

(first entry)

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RESULT 9
ABG18578
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
                                                Novel human diagnostic protein #18569.
                                                                                                                                                                                                   ABG18578 standard; Protein; 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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23-AUG-2000; 2000US-0649167.
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DB; AAS79229.
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                                                                                                                                                                                                                                                                                                                              LCEKDPPT 26
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                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               72.2%;
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (CC for restore normal activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as cod supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. ABG00010-ABG30377 represent novel human
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Matches 6
            Human; chromosome mapping; gene mapping; gene therapy; forension food supplement; medical imaging; diagnostic; genetic disorder
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                                                              Novel human diagnostic protein #19782.
                                                                                                                                      ABG19791;
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23-AUG-2000;
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2000US-0649167.
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RESULT 11
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CC and to produce other data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the purposition and products decreased the content of the printed of the purposition of the printed of the sequences.
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                  Homo sapiens
                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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23-AUG-2000; 2000US-0649167
                                                                                                                  Novel human diagnostic protein #4101
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RESULT 12
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Matches 6
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N-PSDB; AAS68297.
               WO200175067-A2
                                             Homo sapiens.
                                                                            Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic
                                                                                                                             Novel human diagnostic protein #23973.
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23-AUG-2000; 2000US-0649167.
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CC Onte: The sequence data for this patent did not appear in the printed conspectification, but was obtained in electronic format directly from WIPO or information.
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N-PSDB; AAS88169.
                                                                                                                                                                                           Novel human diagnostic protein #25264.
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                                                                                             Homo sapiens
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23-AUG-2000; 2000US-0649167.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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23-AUG-2000; 2000US-0649167.
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                                                                                            11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 LCEKDPPT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LCNEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.2%;
75.0%;
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Pred. No.
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30-MAR-2001; 2001WO-US08631

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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (I) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company in the polypeptide and polymuclectide sequences are useful for treating or disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in company to the polypeptide and polymuclectide sequences have applications in company in the polymuclectide sequences have applications in company in the product of the polymuclectide sequences of the traits to assess biodiversity and to produce other types of data and products dependent on DNA and company in the product sequences of the invention.

CC and no acid sequences of the invention.

CC diagnostic anino acid sequences of the invention.

CC anino acid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cat first the printed specification of the printed spe
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                           28-APR-1998;
                                                                     28-APR-1998;
                                                                                                                  04-NOV-1999
                                                                                                                                                            DE19820190-A1
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                         Pancreas; tumor;
                                                                                                                                                                                                                                                                                                                      Human prostate tumor EST fragment derived protein #344.
                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                              AAY74157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY74157 standard; Protein; 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polypeptide (II) sequences. (I) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 48983; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                           98DE-1020190
                                                                     98DE-1020190
                                                                                                                                                                                                                                                                            EST;
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75.0%;
                                                                                                                                                                                                                                                                         ехргеввеф
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                         sequence tag; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide (I) and suseful as hybridisation probes,
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Search completed: September 10, Job time: 32.95 secs

2003, 17:40:20

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                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                      This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. ANY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library derived expressed sequence tag (EST) sequences represented in
                                                                                                                                                                                                                                                                                             New human nucleic acid sequences from pancreatic tumors,
                                                                                                                                                                                                                                                                                                                            WPI; 1999-621386/54.
N-PSDB; AAZ52971.
                                                                                                          Sequence
                                                                                                                                                    represent protein fragments encoded by library derived expressed sequence tag
                                                                                                                                                                                                                                                        Claim
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                                                                                                                                        AAZ52858-Z53014.
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164 MCDDDPPT 171
                          2 LCNEDPPT 9
                                                                                                                                                                                                                                                     Page 452;
                                                                                                            284 AA;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                     Specht T,
                                                                                                                                                                                                                                                     502pp; German.
                                                                  72.2%;
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                                                     Score 39; DB
Pred. No. 68;
3; Mismatches
                                                                                 20;
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                                                                                Length 284;
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
    6:
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112:
113:
114:
115:
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54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QLCNEDPPT 9
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                              sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
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sp_archeap:*
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sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	0	v	4	w	N	ш	Result No.
39	39	39	39	39	39	39	39	39	39	40	40	40	41	42	44	Score
72.2		72.2	72.2		72.2				72.2	74.1	74.1	74.1	75.9	77.8	81.5	Query Match
404	286	285	285	285	285	268	268	268	267	1068	1051	339	407	1009	227	Query Match Length DB
11	10	10	10	10	10	10	10	10	10	11	11	16	4	w	σ	BB
Q8R0D7	QBLSX4	Q8LSX3	9XST8D	Q8LSX7	Q8LSX5	Q8LSY1	8XST8	OXSTBD	Q8LSX2	Q8R4U7	Q9ESV1	Q8EXZ4	Q8N7X4	074378	Q9N8Y0	ID
Q8r0d7 mus musculu	Q8lsx4 juniperus r	Q8lsx3 chamaecypar	Q8lsx6 thujopsis d	Q81sx7 chamaecypar	-	Q8lsy1 glyptostrob	Q8lsx8 sequoia sem	Q8lsy0 taxodium di	Q8lsx2 chamaecypar	Q8r4u7 mus musculu	Q9esv1 rattus norv	Q8exz4 leptospira	Q8n7x4 homo sapien	074378 schizosacch	Q9n8y0 trypanosoma	Description

ALIGNMENTS

RE O7 ID AC DT	Оу	RE. SOO DATA RADO OS SO
RESULT 2 074378 ID 074378; PRELIMINARY; PRT; 1009 AA. AC 074378; DT 01-NOV-1998 (TrEMBLrel. 08, Created) DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)	Best Local Similarity 87.5%; pred. No. 1; Matches 7; Conservative 1; Mismatches 0 2 LCNEDPPT 9 : 23 LCSEDPPT 30	NORYO Q9NBYO Q9NBYO; Q9NBYO; Q9NBYO; O1-CCT-2000 (TYEMBLYE1. 15, C O1-CCT-2000 (TYEMBLYE1. 15, L O1-WAR-2003 (TYEMBLYE1. 23, L EWARTYOTA; EUGHORE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-TREUS-27; Hall N., Bowmann S., Quail M., Lenmard N.J., Clark L.N., Har Gerrard C., Rajandream M.A., Submitted (JUN-2000) to the E EMBL; AL929604; CAB95403.1; - SINGERY SEQUENCE 227 AA; 25965 MW;

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RESHLT 4
Q8EXZ4
ID Q8EXZ4
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Matches
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Q8N7X4;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                      Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsu Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AK097561; BAC05102.1; -. IRIGIA MAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGRO0239; SEQUENCE 1009 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyne M., Rajandream M.A., Barr
Submitted (AUG-1998) to the EM
EMBL; AL031261; CAA20299.1; --
GeneDB_SPombe; SPBC3H7.03c; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ40242.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-972h-;
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SPBC3H7.03C
Schizosaccharomyces pombe (Fissi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Testis;
                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 4(
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01454; MAGE; 2.
PROSITE; PS50838; MAGE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001017; Dehydrogenase E1.
InterPro; IPR005475; Transketolase_CR.
Ifter Pr00676; E1_dehydrog; 1.
Pfam; Pr00779; transket_pyr; 1.
Pfam; PF02779; transket_pyr; 1.
TIGRPAMs; TIGR00239; 20x0_dh_E1; 1.
SEQUENCE 1009 AA; 114163 MW; 4CB25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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7; Conserv
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6; Conser
                                                                                                                                                                   QLCNEDPP 8
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                                                                                                                      QVCNSDPP
                                                                                                                                                                                                                                                                                                          al protein.
                                                                                                                                                                                                              75.9%;
llarity 75.0%;
Conservative
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         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                        $
                                                                                                                        353
                                                                                                                                                                                                                                                                                                        44091 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fission yeast)
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                                                                                                                                                                                                           Score 41; DB
Pred. No. 7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
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Pred. No.
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         PRT;
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HSSP; P04268; 1IC2.
SEQUENCE 1051 AA; 117175
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Mammalia; Eutheria;
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01-MAR-2001 (TrEMBLrel. 16, Cr
01-MAR-2001 (TrEMBLrel. 23, La
01-MAR-2003 (TrEMBLrel. 23, La
Putative transcription factor
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Hypothetical protein; Complete proteome.
SEQUENCE 339 AA; 39035 MW; A7F815C3EA23CDD9
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sun D.S.,
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a novel leucine :
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A.C., Jenkins N.A.,
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Rodentia;
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85.7%;
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85.7%; Pred. No.
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Sciurognathi;
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chi; Muridae; Murinae; Rat
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01-OCT-2002
01-MAR-2003
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Lee M.W., Chang A.C., Sun D.S., Hsu C.Y., Chang N.C.;
"Restricted Expression of LUZP in Neural Lineage Cells: A Study Embryonic Stem Cells.";
J. Biomed. Sci. 8:504-511(2001).
EMBL; AF362727; AAM00289.1; -
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SEQUENCE FROM N.A.
STRAIN=129/SvJ;
                                InterPro; IPR001005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA_binding; 1.
SMART; SM00717; SANT; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS0090; MYB_3; 1.
                                                                                                                                                                                                                                  Chamaecyparis pisifera.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
Chamaecyparis.
                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR ()
-!- SIMILARITY: CONTAINS 1 MYB-LIKE
EMBL; AB076600; BAB91464.1; -
                                                                                                                                                                                                                                                                                             Myb transcription
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Eukaryota; Metazoa; Chordata; Cr
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                          Kusumi J., Tsumura Y., Yoshimaru H., 'Molecular Evolution of Nuclear Genes
                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21959336; PubMed=11961107;
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Sun D.S., Chang A.C., Jenkins N.A.,
 SEQÜENCE
                    Nuclear protein.
                                                                                                                                   Mol. Biol. Evol. 19:736-747(2002).
                                                                                                                                             Conifer Trees.";
                                                                                                                                                                                                                     NCBI_TaxID=99808;
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85.7%;
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F0FE23272A9299CA CRC64;
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Q8LSXB;
Q8LSXB;
Q1-OCT-2002 (TrEMBLrel. 22, Created)
Q1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 23, Last annotation updat
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation updat
"MOLECULAR TREES.";
CONIÉEY TREES.";
MOI. Biol. Evol. 19:736-747(2002).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NYB-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
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                                                                                                                                                    "Molecular Evolution of
                                                                                                                                                                      MEDLINE=21959336; PubMed=11961107;
                                                                                                                                                                                                                                                         Sequoia sempervirens (California redwood).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Sequoia.
NCBI_TaxID=28980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein.
NON TER 1
SEQUENCE 268 AJ
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SMART; SM00717; SANT; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 1.
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Mol. Biol. Evol. 19:736-747(2002).

-!- SUBCELULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

EMBL; AB076592; BAB91456.1;

InterPro; IPR001005; Myb DNA binding.
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"Molecular Evolution of Nuclear Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21959336; PubMed=11961107;
Kusumi J., Tsumura Y., Yoshimaru H.,
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NCBI_TaxID=28982;
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Coniferopsida; Coniferales;
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KUSUMİ J., TSUMUTA Y., YOSHİMBATU H., TACHİDA H.;

KUSUMİ J., TSUMUTA Y., YOSHİMBATU H., TACHİDA H.;

KUSUMİ J., TSUMUTA Y., YOSHİMBATU H., TACHİDA H.;

MOLEVLAR EVOLULİON OF NUCLEAR GENES İN CUPRESSACEA, A (
CONİFET TREES.";

MOL. BİOL. EVOL. 19:736-747(2002).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C-!- SUBLILARITY: CONTANINS 1 MYB-LIKE DOMAIN.

EMBL, AB076591; BAB91455.1; -.

R INTERPRO IPROLOO5; MYB DNA, BİNDİNG.

R INTERPRO IPROLOO5; MYB DNA, BİNDİNG.

R PROSITE; PSO0334; MYB _2; 1.

R PROSITE; PSO0334; MYB _2; 1.

R NASTITE; PSO0334; MYB _2; 1.
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                                                                            01-OCT-2002
01-OCT-2002
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Thuja standishii.
Eukaryota; Viridiplantae;
Spermatophyta; Coniferopsi
NCBI_TaxID=89194;
                                                    MYB.
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NON TER 1
SEQUENCE 268 A
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
Glyptostrobus.
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Myb transcription factor (Fr
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SMART; SM00717; SANT; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB_3; 1.
                                                               Myb transcription
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Pfam; PF00249; myb_DNA-binding; 1.
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(TrEMBLrel. 22, Last sequence update)
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iption factor (Fragment).
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                                                                                                                              PRELIMINARY;
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            idiplantae; Streptophyta; Embryophyta; Tracheophyta; Coniferopsida; Coniferales; Cupressaceae; Thuja.
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75.0%;
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75.0%;
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(Fragment).
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Pred. No. 11;
1; Mismatches
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RESULT 13
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01-MAR-2003
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"Molecular Evolution of Nuclear Genes in Cupressaci
Conifer Trees.";
Mol. Biol. Evol. 19:736-747(2002).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: COUTAINS 1 MYB-LIKE DOMAIN.
EMBL; AB076597; BAB91461.1;
-- InterPro; IPR001005; Myb DNA binding.
                                                                                                                                                                                                                                                                                  Nuclear protein.
NON TER 1
SEQUENCE 285 A
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conifer Trees.";

Mol. Biol. Evol. 19:736-747 (2002).

-i- SUBCELULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

EMBL; AB076595; BAB91459.1; -.

InterPro; IPR001005; Myb_DNA_binding.
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SEQUENCE FROM N.A.
MEDLINE=21959336; PubMed=11961107;
Tenmura Y., Yoshimaru H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chamaecyparis pisifera.
Eukaryota; Viridiplantae; Streptophyta; Emb
Spermatophyta; Coniferopsida; Coniferales;
Chamaecyparis.
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NON TER 1
SEQUENCE 285 AJ
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SMART; SMO0717; SANT; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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PRELIMINARY;

PRT;

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Q8LSX6; 01-OCT-2002 (TrEMBLrel. 22, Created) 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Myb transcription factor

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Matches 6
     Query Match
Best Local Similarity
                                                                                                       EMBL; AB076599; BAB91463.1; -.
InterPro; IPR001005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 1.
SMART; SM00717; SANT; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB_3; 1.
Nuclear protein.
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01-OCT-2002
01-OCT-2002
01-MAR-2003
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
EMBL; AB076596; BAB91460.1; -.
InterPro; IPR001005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 1.
SMART; SM00717; SANT; 1.
SMART; SM00717; SANT; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS00334; MYB_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21959336; PubMed=11961107;
Kusumi J., Tsumura Y., Yoshimaru H., T
"Molecular Evolution of Nuclear Genes
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MEDLINE=21959336; PubMed=11961107;
Kusumi J., Tsumura Y., Yoshimaru H., T
"Molecular Evolution of Nuclear Genes
                                                                                                                                                                                                                                                                                                                 CONIFER Trees.";

MO1. Biol. Evol. 19:736-747(2002).

NO1. BIOL. EVOL.

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
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Enbryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Thujopsis.
NCBI_TaxID=13727;
                                                                                 SEQÜENCE
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     Score 39;
Pred. No.
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01-OCT-2002
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-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
EMBL; AB076598; BAB91462.1;
                                                                                                                                                                                                                                                                              MEDLINE=21959336; PubMed=11961107;
Kusumi J., Tsumura Y., Yoshimaru H., '
"Molecular Evolution of Nuclear Genes
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Spermatophyta; Coniferopsi
NCBI TaxID=99809;
                                                                                                                                    SEQUENCE
                                                                                                                                               Nuclear protein.
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                                                                                       Local Similarity nes 6; Conserv
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2 (TrEMBLrel. 22, Last seq.
3 (TrEMBLrel. 23, Last annotation factor (Fragment).
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TF3A_MOUSE
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Grimwood J., S	na K	ê.	_ n	. z	Usdin 1	rusina res M F	dan H.,	llins H	Feingo	Skin; PubMed		00) to	Shibahara T., Tanaka T., Nak	wara T.	υ.	00) to	clones	P.P., J	•	2000).	S., de	arcinoma;		a; Cio	an).	eric pi	binding	41, La	ANDARD 9NWR2;			1372	1001	611 731	370	211 256	
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Schmut:	A.C., Sh	n M.,	, Hale S., Garcia A.M., Gay L.J.,	Kernan	, Toshi	Farmei	ore T.,	uetow	.A., G	477932;		the EMBL/GenBank/DDBJ (kamura	no T.,		EMBL/C	th funct	д н. Q.,		•	H I	50490.		s; Cata	2	in Rapi	ctor 2	equenc	PRT;		ALI	INSR_N	NPA2 MOUSE TP3A HUMAN	GHR CO	TPS1_F	NDK5_N	•
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

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RESULT 2
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domains.";
J. Mol. Biol. 3
-1- FUNCTION: 1
                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        DNA_BIND
                                                                                                                                                                                                                                                  PROSITE; PS50172; BRCT; FALSE NEG.
PROSITE; PS50090; MYB_3; FALSE NEG.
Nuclear protein; Chromosomal protein; Telomere;
DOMAIN 78 101 BRCT.
                                                                                                                                                                                                                                                                                                                                                                                   Genew;
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Nishimura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21431821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schnerch A., Schein J.E., Jones S
"Generation and initial analyses";
human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - 1. SUBCELLULAR LOCATION: Nuclear. Colocalizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBUNIT: Homodimer.
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                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                    InterPro; IPR001357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interphase and metaphase cells.
TISSUE SPECIFICITY: Ubiquitous; highly
MISCELLANEOUS: Recruited to telomeres
not directly bind to DNA itself.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 BRCT domain.
SIMILARITY: Contains 1 MyC-like domain.
CAUTION: Ref. 2 sequence differs from that
frameshift in position 151
                                                                                                                                                                                                                                                                                                                   GO:0007003; P:telomere binding; TAS. arPro; IPR001357; BRCT.
                                                                                                                                                                                                                                                                                                                                           GO:0000228; C:nuclear chromosome; TAS GO:0007004; P:telomerase-dependent te
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                                                                                                                                      Similarity
5; Conserv
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May play a role i
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                      STANDARD;
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304
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positive surface charge typical
                                                                                                                                                72.2%;
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                                                                                                                                                                                                                                                                                                        DNA_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ALT_FRAME.
ALT_TERM.
                                                                                                                                                Score 39;
Pred. No.
                                                                                                                                                                                   MYB.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL
Y-> H (IN REF. 3).
Y-> H (IN REF. 3).
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                     PRT;
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SEQUENCE FROM N.A.

MEDLINE-85012734; PubMed=6090949;
Nikaido T., Shimizu A., Ishida N., S
Uchiyama T., Yodoi J., Honjo T.;

"Molecular cloning of cDNA encoding
Nature 311:631-635(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leonard W.J., Depper J.M., Kanehisa M., Svetlik P.B., Sullivan M., Greene W.C.; "Structure of the human interleukin-2 rescience 230:633-639(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Interleukin-2 receptor alpha chain precursor
"""" (CD25 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86067183; PubMed=2999698; MEDLINE=86067183; PubMed=2999698;
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[6]
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Leonard W.J., Depper J.M., Crabtree (
Robb R.J., Kroenke M., Svetlik P.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross S.L., F
Leonard W.J.;
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Shimizu A., Honjo T.;
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                           modelling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95111955; PubMed=7529123; Bamborough P., Hedgecock C.J., Richards W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87159546; PubMed=3030566; Cross S.L., Feinberg M.B., Wolf J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                               "The interleukin-2 and interleukin-4 receptors studied by molecular
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                                                                                                                                 -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
-!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHA EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONO CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO WITH A GAMMA CHAIN.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 2 Sushi (SCR) domains.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD25 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd25.htm".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the human interleukin-2 receptor alpha chain promoter:
of a nonfunctional promoter by the transactivator gene of
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GO:0007166; P:cell surface receptor linked signal transdu.
GO:0006955; P:immune response; TAS.
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F:interleukin-2 recepto
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hodgson G.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Nibler K., Collet S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Hoodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
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RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Sanchez M., del Rey F., Benito J.,
RA Crutal L., Lower T., McCombie W.R., Paulsen I., Potashkin J.,
Thode G., Martin G., Nurse P.,
The General R., Schaler M., Schaler R.,
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C2G11.05c in chromosome
SPACCG11.05C.
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Q1-JUL-1993 (Rel. 26, Created)
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01-FEB-1996 16-OCT-2001

(Rel. 33, (Rel. 40,

2-oxoglutarate (EC 1.2.4.2) (*I*

(Alpha-ketoglutarate

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Query Match
Best Local S
Matches 5
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                                                                                                                                              CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koike K., Urata Y., Goto S.;
"Cloning and nucleotide sequence of the cDNA encoding oxoglutarate dehydrogenase (lippamide).";
Proc. Natl. Acad. Sci. U.S.A. 89:1963-1967(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organization and mapping to chromosome 7p13-p14.";
Gene 159:261-266(1995).
-I- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                           Glycolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The gene encoding human 2-oxoglutarate dehydrogenase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0006091; P:energy pathways; TAS
InterPro; IPR001017; Dehydrogenase E1.
InterPro; IPR05175; Transketolase_CR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS,
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                                                                                                                                                                                                                                                                                                        iterPro; irrover:...
fam; pr00879; l.
fam; pr0279; transket_pyr; l.
fam; Pr0279; transket_pyr; l.
IGRPAMs; TIGR00239; 20x0 dh E1; l.
IGRPAMs; TIGR00239; 20x0 dh E1; l.
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CATALYTIC ACTIVITY: 2-OXOGLUTARATE + lipoamide = S-succinyldihydrolipoamide + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q02218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COFACTOR: THIAMINE PYROPHOSPHATE. ENZYME REGULATION: CATABOLITE REPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:8124;
   Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
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68.5%;
nilarity 71.4%;
Conservative
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1002
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31. 40, Last annotation update)
dehydrogenase E1 component, mitochondrial precursor
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A
                                                                                                                                                                                                                                                    1002
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       <u>ب</u>
Score 37; DB
Pred. No. 45;
2; Mismatches
                                                                                                                                                                           2-OXOGLUTARATE COMPONENT.
N -> D (IN REF.
                                                                                                                                                                                                                                                                                         MITOCHONDRION.
                                                                                                                                              28DAEFC55AC6F763 CRC64;
                                                                                                                                                                        2
                                                                                                                                                                                                                                                    DEHYDROGENASE
       <u>.</u>.
                                                                     Length 1002;
                                                                                                                                                                                   BAA06836]
       Indels
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RESULT 6 IL2A_FELCA

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RESULT 5
IL2A_CANFA
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062802;
30-MAY-2000
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DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.

-!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
-!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
-!- EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY MONOMER (ALPHA AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 2 Sushi (SCR) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-2 receptor alpha chain precursor subunit) (P55) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                        Pfam; PF00084; sushi; SMART; SM00032; CCP;
                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb
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the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dickerson E.B., Padilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9615;
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23 LCDDDPP 29
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               2 LCNEDPP
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                                                 Conservative
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2537
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177
165
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181
30356 I
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CYTOPLASMIC (POTE)
SUSHI 1.
SUSHI 2.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
CHARACTER (GLUNAC.
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                                                           Score 36;
Pred. No.
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EXTRACELLULAR
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                                                  Mismatches
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                                                              DB 1;
16;
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ia; Canidae;
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                                                                                                                                                                                                  (POTENTIAL).
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Canis.
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RESULT 7
TPSB_CAEEL
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                     TPSB CAEEL
Q20351;
30-MAY-2000
30-MAY-2000
30-MAY-2000
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                                                                                                                                                                                                                                  CARBOHYD
SEQUENCE
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P41690;
01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                               TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
Putative protein-tyrosine sulfotransferase (Tyrosylprotein sulfotransferase) (TPST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hasegawa A.;
Submitted (APR-1993) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D16143; BAA03714.1;
HSSP; P01589; 1ILM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-2 receptor alpha chain precursor (IL-2
subunit) (P55) (TAC antigen) (CD25).
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                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsumoto Y., Ohno K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9685;
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Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                     PF00084; sushi; SM00032; CCP;
                                                                                                                                   22 ELCDENPP
                                                                                                                                                          1 QLCNEDPP 8
                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000436; Sushi_SCR_CCP
                                                                                                                                                                                                                                  275
                                                                                                                                                                                                                                              222
2244
263
263
122
122
1525
1525
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
                    (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 32, Created)
                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: Type I membrane protein. Contains 2 Sushi (SCR) domains.
                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                 275
243
262
275
                                                                                                                                                                                                                                              185
67
80
168
184
70
                                                                                                                                                                                             66.7%;
                                                                                                                                                                                                                                  30817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goitsuka R.,
                                                                                                                                                                                                                                  ₩.;
                                                                                                                                                                                                                              SUSHI 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC. . .) (POTENTIAL).
N-LINKED (GLONAC. . .) (POTENTIAL).
N-LINKED (GLONAC. . .) (POTENTIAL).
YM; C97BBDBDD06332326 CRC64;
                                                                                                                                                                                 Score 36; DB
Pred. No. 17;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC
SUSHI 1.
                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Repeat; Signal; Sushi. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                     INTERLEUKIN-2 RECEPTOR AL EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirota Y.,
                                                                       359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
            (E)
                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR ALPHA CHAIN
                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases.
            2.8.2.20)
                                                                                                                                                                                                          Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsujimoto H.,
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
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RESULT
TPST_DR
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                              Matches
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G
                                                                                                                                                                                                                 Q9ŸYB7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable protein-tyrosine sulfotransferase (E
                                                                                                                                                                                          (Tyrosylprotein sulfotransferase) CG32632/CG1573.
                                                                                                                                                                                                                                                                                 TPST
                                                                                                                                                                                                                                                                                             DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transferase; Transmembrane; Glycoprotein; Signal-anchor.

DOMAIN 1 27 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U00051; AAA91354.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                        STRAIN=Berkeley
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                         Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00685; Sulfotransfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WormPep; F42G9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taich A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T16350; T16350
                                                                                                                                                                                                                                                                                 DROME
                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                     1 QLCNEDPPT
                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                               RLCNKDPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000863; Sulfotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                359
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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28
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                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
66.7%;
                                                                                                                                                                              (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                                                  sulfotransferase (EC
                                                                                                                                       Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                LUMENAL, CATALYTIC 9FC2F44539B8CC53
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                    Brachycera;
                                                                                                                                                                                                                                                                                 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                              1:
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 359;
                                                                                                                                                                                                                   2.8.2.20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                               Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collaboration
  G.L.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non
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TPSA_CAEEL
ID TPSA_CAEEL
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                                                                                          Matches
                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                        EMBL; AE003493; AAF48286.1;
                                                                                                                                                                                                                                                                                                                                                        ACIDIC MOTIFS OF POLYPEPTIDES (BY SIMILARITY).
--- CATALYTIC ACTIVITY: 3'-phosphoadenylylenlfate + protein tyrosine adenosine 3',5'-bisphosphate + protein tyrosine-0-sulfate.
---- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (F
                                                                                                                                                                                       Hypothetical p
Signal-anchor.
                                                                                                                                                                                                            Pfam; PF00685; Sulfotransfer; 1.
                                                                                                                                                                                                                                                                                                                                     - 1- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY
                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                 similarity).
                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.F.
                                                                      1 QLCNEDPPT
                                                                                         6; Conserv
                                                   RLCNKDPLT 164
                                                                                                                            31
362
385
                                                                                                                                                                                                                     :PR000863; Sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agbayani A.,
                                                                                          Conservative
                                                                                                                                                                      10
                                                                                                                                                                                                 protein; Transferase; Transmembrane; Glycoprotein;
                                                                                                                               ₽
     STANDARD;
                                                                       9
                                                                                                                                         385
370
                                                                                                                                                                    30
9
                                                                                                                               44054 MW;
                                                                                                  66.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An H.-J., Andrews-Pfannkoch C.,
                                                                                                  Score 36;
Pred. No.
                                                                                                                                                                    CYTOPLASMIC (POTENTIAL) .
SIGNAL-ANCHOR (TYPE-II N
                                                                                                                                                 LUMENAL,
                                                                                                                                                             (POTENTIAL)
     PRT;
                                                                                                                               35BAE2B3E2D2FE1C CRC64;
                                                                                          Mismatches
     380
                                                                                                                                                  CATALYTIC (POTENTIAL)
                                                                                                           1,
                                                                                                                                                                      (TYPE-II MEMBRANE PROTEIN
                                                                                         1;
                                                                                                           Length 385
                                                                                         0,
                                                                                         Gaps
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RESULT 10
TE2I_MOUSE
                                                                                                                                                                                 PAC IS
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                                                                                                                                 Query Match
Best Local S
Matches 6
                                                                                                                                                                                 DOMAIN
CARBOHYD
SEQUENCE
TE2I MOUSE STANDARD;
Q91VL8; Q9JJE8; Q9JJE9;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is published between the Swiss Institute of Bioinformatic the Swiss Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and expression of human and mouse tyrosylprotein sulfotransferase-2 and a tyrosylprotein sulfotransferase homologue: Caenorhabditis elegans.";
J. Biol. Chem. 273:24770-24774(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein-tyrosine sulfotransferase A (EC 2.8.2.
sulfotransferase-A) (TPST-A).
                                                                                                                                                                                                                                                                                                     EMBL; AF049709; AAC36062.1; -.
EMBL; AL132904; CAC35844.1; -.
PIR; T42755; T42755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                    MOUSE
                                                                                                                                                                                                                                                                   WormPep; Y111B2A.15; CE26632.
InterPro; IPR000863; Sulfotransferase.
Pfam; PF00685; Sulfotransfer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Durbin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=98406128; PubMed=9733778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O77081; Q9NEW9;
                                                                                                                                                                                                                               Transferase; Transmembrane; Glycoprotein; Signal-anchor.

DOMAIN
1 6 CYTOPLASMIC (POTENTIAL).

TRANSMEM 7 27 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
-!- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouyang Y.-B., Moore K.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y111B2A.15
                                                                                    155
                                                                                                           1 QLCNEDPPT
                                                                                                                                 Similarity 6; Conserv
                                                                                    RLCNKDPFT
                                                                                                                                                                             28
66
380
                                                                                                                                   Conservative
                                                                                                                                                                                  ₽
                                                                                    163
                                                                                                           9
                                                                                                                                                                                             380
                                                                                                                                                                                  43313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nematoda;
                                                                                                                                              64.8%;
                                                                                                                                                                                  M. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oda; Chromadorea; Rhabditida; Rhabditoidea; Caenorhabditis
                                                                                                                                               Score
Pred.
                                                                                                                                                                                             LUMENAL, CATALYTIC (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENT
                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                  FF709BF00F1EDC95 CRC64;
                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                ght. It is produced through Bioinformatics and the EM
                                                                                                                                                35;
                          393
                                                                                                                                                                                                                                                                                                                                                                  moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                    There are no
                                                                                                                                                                                                                                                                                                                                                                                          as its content
                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20) (Tyrosylprotein
                                                                                                                                                        Length 380
                                                                                                                                    Indels
                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESIDUES WITHIN
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                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                             collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cararinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Tennan and mouse cDNA sequences."
RT Thuman and mouse cDNA sequences."
RT. Torca Narl Acad. Sci. U.S. A. 99-16899-16901(2002)
                                                                                                                                                                                                                                                                                                     EMBL; BC012270; /
EMBL; BC017641; /
EMBL; AB041557; F
EMBL; AB041559; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation of full-length cDNA clones from mouse brain made by oligo-capping method.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                    DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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15-SEP-2003 (Rel. 42, Last annotation update)
Telomeric repeat binding factor 2 interaction
interacting telomeric protein Rapl).
                                                                                                                                                            InterPro; IPR001357; BRCT
InterPro; IPR001005; Myb DNA bindin
PROSITE; PSS0172; BRCT; FALSE NEG
PROSITE; PS50090; MYB_3; FALSE_NEG;
                                                                                                                                                                                                                                                                        MGD; MGI:1929871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osada N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TERF2IP OR RAP1
                                                                                                              DOMAIN
                                                                                                                                     Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hashimoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-280 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 BRCT domain.
SIMILARITY: Contains 1 Myb-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: May play a role in telomere SUBUNIT: Homodimer. Binds to TRF2 (but
                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kusuda J., Tanuma R.,
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232
377
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                                                                                                                                                                                                                                                                                                                            ; AAH12270.1; -.; AAH17641.1; -.; BAA95042.1; -.
                                                                                                                                                                                                                                                                                                     BAA95043.1; ALT_INIT
                                                                                                                                  Chromosomai
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                                                                                                                                                                                                                                                                           Terf2ip.
                          101
185
297
393
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                    DNA_binding
MYB.
ASP/GLU-RICH (ACIDIC)
NUCLEAR LOCALIZATION
                                                                                                                                     protein; Telomere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ito A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colocalizes with telomeric
                          LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length regulation.
: not TRF1) with its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
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Best Local S
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCS3_RABIT
Q9TT17;
 TRANSMEM TRANSMEM
                        Multigene .
                                                                                    Pfam; PF00520; ion_trans; 1.
Pfam; PF02214; K tetra; 1.
PRINTS; PR0169; KCHANNEL.
PRINTS; PR01494; KV9CHANNEL.
PRINTS; PR01491; KVCHANNEL.
                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Potassium channel subunit. Modulates char and reduces the ion flow (By similarity).
-!- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                             EMBL; AF209723; AAF22833.1;
InterPro; IPR000210; BTB_PO
                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rae J.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         channel Kv9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potassium
                                                                          SMART; SM00225;
                                                                                                                                                        InterPro;
                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9986;
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                                                                                                                                                                               InterPro;
                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                      every third position.
SIMILARITY: BELONGS :
                                                                                                                                                                                                                                                                                                                                                                                                             plasma membrane but remain in an intracellular compart absence of KCNB1 (By similarity) the voltage-sensor DOMAIN: The segment S4 is probably the voltage-sensor characterized by a series of positively charged amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homomultimers. Might also
                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced een the Swiss Institute of Bioinformatics and
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5; Conserv
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                                                                                                                                                                                   o; IPR000210; BTB POZ.
b; IPR005821; Ion_trans.
c; IPR001622; K+channel_pore.
c; IPR003091; K_channel.
c; IPR003131; K_tetra.
c; IPR003131; K_tetra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCDGDPPT
                                                                                                                                                                                                                                                                                                                        non-profit institutions as long
                                                                                                                                                 IPR003971; KV9_channel.
IPR003968; KV_Channel.
IPR005820; M+Channel_nlg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03 (Rel. 41, Last sequence update)
03 (Rel. 41, Last annoctation update)
voltage-gated channel subfamily S member 3 (Potassium
v9.3) (Delayed-rectifier K+ channel alpha subunit 3).
                                      family.
                                                  channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
393 AA;
                                                  Ion transport; Ionic channel; Voltage-gated channel;
channel; Potassium; Potassium transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zealand
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                                                                            BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      white; TISSUE=Corneal epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286
 185
206
244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                       TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.
                                                                                                                                                                                                                                                     .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35;
Pred. No.
CYTOPLASMIC (POTENTIAL)
SEGMENT S1 (POTENTIAL).
SEGMENT S2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTPEED -> HTHTQS (IN REF. 7A15CFD83733BE2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to other
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                                                                                                                                                                                                                                                                                                                        as its content
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Best Local S
Matches 5
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Potassium voltage-gated channel subfamily S member 3 (Potassium Potassium voltage-gated channel subfamily S member 3 (Potassium Voltage-gated channel subfamily S member 3).
                                                       This SWI
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TRANSMEM
DOMAIN
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TRANSMEM
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           between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                  alpha-subunits cloned from rat brain.",
Biophem. Biophys. Res. Commun. 248:927-934 (1998).
Biochem. Biophys. Res. Commun. bubunit. Modulates
-i-FUNCTION: Pocassium channel subunit. Modulates
and shifts the activation threshold of KCNB1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patel A.J., Lazdunski M., Honore E.; "Kv2.1/Kv9.3, a novel ATP-dependent delayed-rectifier K+oxygen-sensitive pulmonary artery myocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Brain, and Kidney;
MEDLINE-98031889; PubMed-9362476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
 entities
                                                                                                                                                                                                                                                                                                                                                                         "Cloning and tissue distribution of two new potassium
                                                                                                                                                                                                                                                                                                                                                                                         Stocker M.,
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98369652; PubMed=9704029;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 16:6615-6625(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                      SSUE-Brain;
                                                                                                              TISSUE SPECIFICITY: Detected in lung, spleen, brain and heart. DOMAIN: The segment $4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.

### SCELLANEOUS: Inhibited by 4-aminopyridine (4-AP). Channel activity is reversibly inhibited by hypoxia and down-regulated the absence of intracellular ATP.
                                                                                                  SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY.
                                                                                                                                                                                                                                                                        SUBUNIT: Heteromultimer with homomultimers. Might also bir
                                                                                                                                                                                                                 absence of KCNB1 (By similarity).
                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. May not reach the plasma membrane but remain in an intracellular compartment in the
                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                                                                                                         values.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAT
                                                                   SWISS-PROT entry is copyright. It is
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                         Kerschensteiner D.;
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statement
a license
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SEGMENT S4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S5 (POTENTIAL).
SEGMENT H5 (PORE-FORMING)
SEGMENT S6 (POTENTIAL).
agreement
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                                                       of Bioinformatics
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CYTOPLASMIC (POTENTIAL)
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2EE396E0889D6F77 CRC64;
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(See http://www.isb-sib
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                      There are no restrictions ng as its content is in
                                                     produced through a collaboration atics and the EMBL outstation -
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 RESULT 13
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Best Local
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Q979L9;
28-FEB-2003
28-FEB-2003
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CONFLICT
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DOMAIN
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Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01494; KV9CHANNEL.
PRINTS; PR01491; KVCHANNEL.
                                 sequence of Thermoplasma volcanium.";

Proc. Natl. Acad. Sci. U.S.A. 97:14252-14262(2000).

-I-FUNCTION: Allows the formation of correctly charged Gln-tRNA(Gln) through the transamidation of misacylated Glu-tRNA(Gln) in
                                                                               Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Ka
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
                                                                                                                                                                                                                  Thermoplasma volcanium.
                                                                                                                                                                                                                             GATE OR TV1141 OR TVG1166951.
                                                                                                                                                                                                                                           subunit
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EMBL; Y17607; C.
                                                                                                                               MEDLINE=20570466; PubMed=11121031;
                                                                                                                                               STRAIN=GSS1
                                                                                                                                                                              NCBI_TaxID=50339;
                                                                                                                                                                                          Thermoplasmataceae;
                                                                                                                                                                                                       Archaea;
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                                                                                                                                                          SEQUENCE
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organisms which lack glutaminyl-tRNA synthetase. takes place in the presence of glutamine and ATP activated gamma-phospho-Glu-tRNA(Gln). The gatDE
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j IPR005821; Ion_trans-
j IPR005821; K+channel_pore.
j IPR003091; K_channel.
j IPR003111; K_tetra.
j IPR003971; KV_channel.
j IPR003968; KV_channel.
j IPR003968; KV_channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                      Euryarchaeota;
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DSM 4299 / JCM 9571;
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                                                                                                                                                                                                                                                                                                                STANDARD;
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    Last sequence update)
    Last annotation update)
    amidotransferase subunit E

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83.3%;
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SEGMENT S4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S5 (POTENTIAL).
SEGMENT H5 (PORE-FORMING).
SEGMENT S6 (POTENTIAL).
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                                                                                                                                                                                                    Thermoplasmatales;
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The reaction through an system is
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                                                                                  genomic
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RESULT 14
DPB2_YEAST
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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

C STRAIN=S288c / AB972;

X MEDLINE=97313271; PubMed=9169875;

X MEDLINE=97313271; PubMed=9169875;

X MEDLINE=97313271; PubMed=9169875;

X A Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

X A Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

X Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,

X Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

X Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

X Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

X A Dietrich F.S., Delius H., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

X A Dietrich F.S., Delius H., Jipaolo T., Kleine K.,

X A Duncan M., Floeth M., Fortin N., Hilbert H., Hillier L.,

X A Duncan M., Floeth M., Fortin N., Hilbert H., Hillier L.,

X A Duncan M., Floeth M., Fortin N., Hilbert H., Hillier L.,

X A Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

X A Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

X A Dietrich F.S., Delius H., Jipaolo E., June B., Lin D., Louis E.J.,

X A Dietrich F. K., Messenguy F., Mewes H., Lin A., Lin D., Louis E.J.,

X A Marathe R., Messenguy F., Mewes H., Wirtipati S., Moestl D.,

X A Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,

X A Petel F.X., Pohl T.M., Purnelle D., Schaffer M., Scharfe M.,
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Best Local S
Matches 5
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724482 (206622;
01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit B).
DPB2 OR YPR175W OR P9705.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=YHA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01234; GĀTB; 1.
Protein biosynthesis; Ligase; Complete proteome.
SEQUENCE 598 AA; 67355 MW; 6777EB8F039F8CCF CRC64;
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InterPro; IPR004413; G
InterPro; IPR006107; G
InterPro; IPR006075; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                               Araki H., Hamatake R.K., Johnston L.H., Sugino A., "DPB2, the gene encoding DNA polymerase II subunit chromosome replication in Saccharomyces cerevisiae. Proc. Natl. Acad. Sci. U.S.A. 88:4601-4605(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
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similarity)
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SUBUNIT: Heterodimer of gatD and gatE (By similarity).
SIMILARITY: BELONGS TO THE GATB/GATE FAMILY. GATE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
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83.3%;
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Pred. No. 60;
1; Mismatches
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RESULT 15
SRB9_YEAST
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Best Local S
Matches 6
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P38931;
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CONFLICT
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SEQUENCE
                   Hengartner C.J., Thompson C.M
Koleske A.J., Okamura S., You
"Association of an activator
Genes Dev. 9:897-910(1995).
                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updats
Suppressor of RNA polymerase B SRB9 (SCA1 p
SRB9 OR SCA1 OR SSN2 OR YDR443C.
              Genes
[2]
                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Zhong W.W., Zollner A., Vo D.H., Hani J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF04042; DNA pol E B; 1.
Transferase; DNA-directed DNA
DNA-binding; Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M61710; AAA34576.1; ALT_INIT.
EMBL; U25842; AAB68109.1; -.
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SEQUENCE FROM N.A
                                                                      MEDLINE=95293223;
                                                                                    STRAIN=S288c
                                                                                              SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: TO OTHER SPECIES DNA POLYMERASE EPSILON, SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kDa, AND 29 kDa).
SUBCELLULAR LOCATION: Nuclear.
MISCELLABOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE
DIFFERENT REACTIONS OF DNA SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITE 387:103-105(1997).
FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
FUNCTION: ODBO TS RESENTIAL FOR CELL GROWTH. MAY HAVE A ROLE
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S0006379; DPB2
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                               ; PubMed=7774808; Thompson C.M., Zhang J., amura S., Young R.A.; an activator with an RNA [
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K -> R (IN REF. 1).
V -> F (IN REF. 1).
E -> Q (IN REF. 1).
T -> I (IN REF. 1).
W; SC01647BD2B6A39A CRC64;
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Pred. No.
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                                  RNA polymerase
                                                                                                                                                                                               update)
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                                                          Chao D.M.,
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                                                           S.-M.,
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Best Local Similarity
Matches 6; Conserv
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EMBL; U09176; AAA18614.1; -.
EMBL; U33007; AAB64875.1; -.
PIR; B57062; B57062.
TRANSFAC; T02153; -.
SGD; S0002851; SSN2.
                                                                                                                             DOMAIN
CONFLICT
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SEQUENCE
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Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Wilson A., Yelton M., Botstein D., Davis R.W., Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COMPONENT OF THE RNA POLYMERASE II HOLOENZYME AND THE MEDIATOR OF ACTIVATION SUBCOMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license sgreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yuryev A., Corden J.L.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear (Potential).
985 KLTNEDPP 992
                       1 QLCNEDPP 8
                                                                                                                                                                                                                                                                                                                         protein
                                                                 Conservative
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75.0%;
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D -> E (IN REF. 2).

E -> V (IN REF. 2).

T -> S (IN REF. 2).

VK -> GE (IN REF. 2).

T -> P (IN REF. 2).

Y -> S (IN REF. 2).

Y -> S (IN REF. 2).
                                                                                                                              WW.
                                                                              Score 35; DB 1;
Pred. No. 1.6e+02;
                                                               Mismatches
                                                               1; Indels
                                                                                             Length 1420;
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Search completed: September 10, 2003, 17:40:53 Job time : 10 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen

Ltd

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Result
No.
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Listing first
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Match
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Gapop 10.0 ,
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1: pir1:*
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177	177	175	174	173	169	168	168	168	163	161	161	161	131	112	1928
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T08126	S04728	S43894	S71554	S47171	F87713	B24620	C24620	A24620	T04989	T52399	H84518	E85354	PH1226	S19971	JS0610
.pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	gene PR-1 protein	conserved hypothet	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	PR-1-like protein	Ig kappa chain pre	Ig kappa chain V r	beta-galactosidase

ALIGNMENTS

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A;Molecule type: mRNA
A;Residues: 1-102 <LIUS
A;Residues: 1-102 <LIUS
A;Cross-references: GB:S46006; NID:g1679976; PIDN:AAB19408.1; PID:g233226
A;Experimental source: prostate bone metastasis cell line PC3
A;Experimental source: prostate bone (NCBIN:46006, NCBIP:46012)
A;Note: sequence extracted from NCBI backbone (NCBIN:46006, NCBIP:46012)
C;Keywords: fusion protein
F;1-50/Region: retrovirus-like H3 promotor region derived
F;51-102/Region: human calbindin derived (fragment)
                                                                                                                                                                                                                                                                                                   R;Liu, A.Y.; Abraham, B.A. Cancer Res. 51, 4107-4110, 1991
A;Title: Subtractive cloning of a hybrid human endogenous retrovirus and calbindin gene A;Reference number: A37413; MUID:91309099; PMID:1713126
A;Accession: A37413
                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical RTVL-H3 promoter region/calbindin fusion protein - C;Species: Homo sapiens (man) C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change C;Accession: A37413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
A37413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosevidues: 1-1009 <LYN>
A;Residues: 1-1009 <LYN>
A;Cross-references: EMBL:AL031261; PIDN:CAA20299.1; GSPDB:GN00067; SPDB:SPBC3H7.03c
A;Experimental source: strain 972h-; cosmid c3H7
A;Experimental source: strain 972h-; cosmid c3H7
Query Match
Best Local Similarity
6; Conserv
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submitted to the EMBL Data Library, Aug
A;Reference number: Z21926
A;Accession: T40412
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C; Superfamily:
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7; Conserve
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                        Conservative
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%; Pred. No. 11;
0; Mismatches
                        ۲.
                     Score 39; DB Pred. No. 3.9; 1; Mismatches
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gust 1998
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                   1.
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A;Molecule type: mRNA
A;Residues: 1-272 <NIK>
A;Residues: GB:X01057; GB:X01058; GB:X01402; NID:g33812; PIDN:CAA25525.1; PID:g3
A;Cross-references: GB:X01057; GB:X01058; GB:X01402; NID:g33812; PIDN:CAA25525.1; PID:g3
R;Cossman, D.; Wignall, J.; Lewis, A.; Alpert, A.; Cerretti, D.P.; Park, L.; Dower, S.K.;
Mol. Immunol. 23, 935-941, 1986
A;Title: High level stable expression of human interleukin-2 receptors in mouse cells ge
A;Reference number: I57801; MUID:87064653; PMID:3097520
                                                                                                                                                                                                    A;Cross-references: GB:X03131; NID:g33818; PIDN:CAA26906.1; PID:R;Nikaido, T.; Shimizu, A.; Ishida, N.; Sabe, H.; Teshigawara, K Nature 311, 631-635, 1984
A;Title: Molecular cloning of cDNA encoding human interleukin-2 A;Reference number: A01856; MUID:85012734; PMID:6090949
A;Accession: A01856
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Crobb-references: GB:M10322
R;Ishida, N.; Kanamori, H.; Noma, T.; Nikaido, T.; Sabe, H.; Suzuki, Nucleic Acids Res. 13, 7579-7589, 1985
A;Title: Molecular cloning and structure of the human interleukin 2 A;Reference number: A24113; MUID:86067183; PMID:2999698
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A; Residues: 1-272 <ISH>
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Science 230, 633-639, 1985
A;Tille: Structure of the human interleukin-2 receptor gene.
A:Reference number: A44186; MUID:86018868; PMID:2996141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: CD25; Tac antigen
N;Contains: interleukin-2 receptor alpha chain, splice form
C;Species: Homo sapiens (man)
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N;Alternate names: CD25; Tac antigen
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Best Local S
Matches 6
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;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000;
;Accession: A44186; A24113; A01856; I57801; I52791; A61346; A33651; A34186;
;Leonard, W.J.; Depper, J.M.; Kanehisa, M.; Kroenke, M.; Peffer, N.J.; Svetl
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;Residues: 1-490 <W
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| Rperimental source: strain 972h-; cosmid c2D10
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esidues: 1-272 <LEO>
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85.7%;
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ra, K.; Maeda,
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Query Match
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A;Status: Lienzane MRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residuse: 22-125, 'K', 127-262,'Q', 264-272 <COS>
A;Cross-references: GB:M14098; NID:g186307; PIDN:AAA5
A;Cross, S.L.; Feinberg, M.B.; Wolf, J.B.; Holbřook,
P.Cross, S.L.; Feinberg, M.B.; Wolf, J.B.; Holbřook,
F;22-272/Product: interleukin-2 receptor alpha chain #status experimenta.
F;22-240/Domain: extracellular #status predicted <EXT>
F;22-194,219-272/Product: interleukin-2 receptor alpha chain, splice for F;22-88,119-87/Region: interleukin-2 binding core
F;22-88,119-87/Region: interleukin-2 binding core
F;125-184/Domain: complement factor H repeat homology <FH2>
F;125-184/Domain: transmembrane #status predicted <TMM>
F;241-259/Domain: intracellular #status predicted <TMN-
F;260-272/Domain: intracellular #status predicted <INT-
F;241-259/Domain: intracellular #status predicted <INT-
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F;24
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A;Map position: 10p15-10p14

A;Introns: 22/1; 86/1; 123/1; 195/1; 219/1; 243/1; 265/2
C;Complex: The high affinity receptor is a heterotrimer of alpha, C;Function:
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A;Residues: 22-26,58-62;109-113;119-123;162-166 <MIE2>
A;Residues: 22-26,58-62;109-113;119-123;162-166 <MIE2>
A;Rote: use of recombinant protein and proteolysis allowed the au
A;Mercken, L.; Moras, V.; Hemon, L.; Lionne, B.; Bousseau, A.; Da
Biochem. Biophys. Res. Commun. 180, 1390-1395, 191
Biochem. Biophys. Res. Commun. 180, 1390-1395, 191
A;Title: An exon 5-deleted mRNA encodes a functional interleukin
A;Reference number: I52255; MUID:92062171; PMID:1840490
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J. Biol. Chem. 264, 21097-21105, 1989
A;Tile: Limited proteolysis of recombinant human soluble A;Reference number: A34186; MUID:90078206; PMID:2687272
A;Accession: A34186
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A;Residues: 22-31 <URD>
R;Residues: C2-31 <URD>
R;Miedel, M.C.; Hulmes, J.D.; Weber, D.V.; Bailon, P.; Pan, Y.C.E.
Biochem. Biophys. Res. Commun. 154, 372-379, 1988
A;Title: Structural analysis of recombinant soluble human interleukin-2 receptor. Primar
A;Reference number: A33651; MUID:88280794; PMID:3134887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: receptor for interleukin-2
A;Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, C;Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology.
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R;Urdal, D.L.; March, C.J.; Gillis, S.; Larsen, A.; Dower, S.K.
Proc. Natl. Acad. Sci. U.S.A. 81, 6481-6485, 1984
A;Title: Purification and chemical characterization of the receptor for interleukin
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A;Title: Regulation of the human interleukin-2 receptor alpha chain promoter: activation A;Reference number: 152791, MUID:87159546; PMID:3030566
A;Accession: 152791
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F;1-21/Domain: signal sequence #status predicted <SIG>
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A; Residues: 193-194, 219-220 < MER >
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A; Residues: 1-21 < CRO>
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Holbrook, N.J.; Wong-Staal, F.; Leonard,
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70.4%; 62.5%;

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m N_7Alternate} names: 2-oxoglutarate:lipoamide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F24M12.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear.cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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                                              C;Species: Homo sapiens
C;Date: 31-Dec-1993 #seq
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A;Note: F24M12.110
              C;Accession: A38234
R;Koike, K.; Urata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; submitted to the Protein Sequence Database, December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T38571;
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                                                                                                                                                                                                                                                                                                                                  Map position: 3
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Accession: T38571
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Accession: T45738
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esidues: 1-895 <VIT>
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Control control cultivar Columbia;
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ta, Y.; Goto,
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A; Introns: 27/3 C; Superfamily:
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A;Cross-references: EMBL:AL355933; GSPDB:GN00116; NCSP:B8B20.370
A;Experimental source: BAC clone B8B20; strain OR74A
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(;Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding C;Keywords: mitochondrion; oxidoreductase; thiamin pyrophosphate; tricarboxylic acid F;1-40/Domain: transit peptide (mitochondrion) #status predicted <TMP>
F;41-1003/Product: oxoglutarate dehydrogenase (lipoamide) #status predicted <MAT>
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A;Cross-references: GB:D10523
A;Experimental source: fetal liver
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                                                                           A;Residues: 1-245 <WIL>
A;Cross-references: EMBL:AL032637; PIDN:CAA21609.1;
                                                                                                                                                    submitted to the EMBL Data Library, A;Reference number: Z20279
A;Accession: T26868
                                                                                                                                                                                                                                             hypothetical protein Y43F8C.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                               T26868
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A; Introns: 27/3; 843/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Schulte, U.; Aign, V.; submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable oxoglutarate dehydrogenase precursor [imported] N; Alternate names: protein BBB20.370
                                                        A; Experimental source: clone Y43F8C
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                                                                                                                                                                                                                                                                                                                                 RESULT 9
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                                                                                                                 A;Molecule type: DNA
                                                                                                                                  A; Status: preliminary; translated from
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streptomycin 3-kinase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
C;Accession: C75518
                                                                                                                                                                                                                                                                                                  Reference number: Z16652

Ccession: T16677

Clession: Lype: DNA

Ccession: 1-185 <BEV >

A;Cross-references: EMBL:AL080283; GSPDB:GN00062; ATSP:F3L17.40

A;Experimental source: cultivar Columbia; BAC clone F3L17
                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogenesis-related protein homolog F3L17.40 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:F42G9.8
A;Introns: 28/2; 50/2; 113/2; 155/3; 220/3; 290/2
C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Taich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                            RESULT 12
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A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, March A;Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                            Bevan, M.; Murphy, G.; Ridley, P.; Hudson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: T16350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Caenorhabditis elegans;Date: 20-Sep-1999 #sequence_rev;Accession: T16350
                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                           Superfamily: pathogenesis-related leaf protein
                                                                                                                                                                                                                                                                         Gene: ATSP:F3L17.40
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Best Local .
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75.0%;
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Pred. No. 34;
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Pred. No. 39;
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A;Molecule type: DNA
A;Residues: 1-283 <WHI>
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A; Note: SPAC3A11.1
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                                                              A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-334 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z17303
A; Accession: T11633
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               Query Match
Best Local :
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 Similarity 6; Conserv
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               64.8%;
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Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                J. Biol. Chem. 273, 24770-24774, 1998
A;Title: Molecular cloning and expression of human and rA;Reference number: Z22262; MUID:98406128; PMID:9733778
A;Accession: T42755
                                                                                                                                                                                                                                                                                                                          tyrosylprotein sulfotransferase homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-380 <MOO>
                                                                                                                                                                                                                                                       R;Moore, K.L.; Ouyang, Y.B.
J. Biol. Chem. 273, 24770-24774, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Barrell, B.G.; Rajandream, M.A.; I submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 1
C; Superfamily: streptomycin 6-kinase
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A;Experimental source: strain R1
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                                                                                            EMBL: AF049709; NID: g3617847; PIDN: AAC36062.1;
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75.0%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.A.; Wood, V.
ibrary, September 1997
Score 35; DB
Pred. No. 81;
2; Mismatches
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                                              DB 2;
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T.; Zalewski, C.; M:
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Match Length
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sp_phage:*
sp_plant:*
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sp_virus:*
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                                Q8DCL2
Q972D4
Q978H7
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Q8PKD3
Q9EWT9
Q9GUY2
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           Q8DRS
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O02369 chironomus
Q8zn46 salmonella
Q8z447 salmonella
Q9h616 homo sapien
Q9h616 homo sapien
Q9hc19 homo sapien
Q8dvu3 streptococc
Q9nxv7 homo sapien
Q8iy21 homo sapien
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Q8iy21 homo sapien
Q8iy21 wibrio vuln
Q97244 sulfolobus
Q97244 sulfolobus
Q9q8h7 myxoma viru
Q8pkd3 xanthomonas
Q9ewt9 streptomyce
Q9guy2 polyandroca
Q8dre5 streptococc
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O86594 streptomyce	086594	16	293	60.0	33	Ü
*	Q8U864	16	249	60.0	33	4
Q9apr9 carboxydoth	Q9APR9	N	178	60.0	33	س
Q98gl3 rhizobium l	Q98GL3	16	174	60.0	33	N
O15588 entamoeba h	015588	ഗ	167	60.0	33	Н
	Q8TK61	17	153	60.0	ω G	0
	Q94B31	10	148	60.0	33	Ö
	Q9LER7	10	148	60.0	33	80
	Q96GJ9	4	134	60.0	33	7
Q9f8j2 carboxydoth	Q9F8J2	N	99	60.0	33	ō
	Q8CVT2	16	1653	61.8	34	Ü
Q8xa93 escherichia	Q8XA93	16	1653	61.8	34	4.
Q935p3 salmonella	Q935P3	16	893	61.8	34	ũ
Q915u7 salmonella	Q9L5U7	N	893	\rightarrow	34	N
m	Q9RGU0	N	887	61.8	34	Ë
	Q8RWQ0	10	880	61.8	34	Ö
	Q9FID9	10	880	61.8	34	Ö
	Q8REC9	16	812	61.8	34	ã
Q9hid7 thermoplasm	Q9HID7	17	767	61.8	34	7
Q53362 acetobacter	Q53362	N	742	61.8	34	õ
Q8kzs8 acetobacter	Q8KZS8	Ν.	742	61.8	34	ហ៊
	Q91VI2	ï	391	\mathbf{L}	34.	4
Q92tr9 rhizobium m	Q92TR9	16	314	\mathbf{L}	34	ũ
Q50403 methylobact	Q50403	N	192	61.8	34	ຄ
_	Q8W1P1	10	1216	63.6	35	ŭ
	Q8IPL3	ភ	556	w	35	õ
ຜ	Q9RN63	N	432	u	35	ø
Q91bd6 spodoptera	Q91BD6	12	363	w	35	œ
Q9x7p7 streptomyce	Q9X7P7	16	345	63.6	35	7

ALIGNMENTS

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Query Match 70.9%; Score 39; DB Best Local Similarity 72.7%; Pred. No. 5.5; Matches 8; Conservative 1; Mismatches	KW Heme; Oxygen transport; Transport. SQ SEQUENCE 167 AA; 18428 MW; 551F5A5DFC3E		DR PRINTS; PR00611; ERYTHCRUORIN.	DR Pfam; PF00042; globin; 1.	DR InterPro; IPR000971; Globin.			EMBL; A	_	in Two Insect Species.";	"Evolution of Orthologous Intronless and			J. Mol. Evol. 38:241-249(1994).	"Intron-containing alobin genes in the				OX NCBI TaxID=7155;	Or Objects, Discopresiyacts, Discopresia			GN CTT-12.	DE Globin XII.	(TrEMBLrel. 22,	Last		AC 002369;	02369 PRELIMINARY; PRT;	RESULT 1 002369
70.9%; Score 39; 72.7%; Pred. No. vative 1; Mismat	transport; Transport. 57 AA; 18428 MW; 551F5A5DFC3E7742 CRC64;	033; GLOBIN; 1.	11; ERYTHCRUORIN.	2; globin; 1.	000971; Globin.	002336; Erythcrurin.	1ECA.		0:0-0(1997).	•	Ø	(ao WY., Bergtrom G.;	N.A.	THE CHIC THEOCOL CHITT CHOMAD		witt P.M. Bergtrom G.:	3867; PubMed=8006991;	N.A.	155;	Thiraneidae. Thiraneidae. Thiraneidae.	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	nummi thummi (Midge).			22, Last	04,	04,			
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01-MAR-2002
01-MAR-2002
                   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:688-852 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8ZN46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE008815; AAL21426 1;
Lipoprotein; Hypothetical pr
SEQUENCE 1644 AA; 179646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8Z4N7;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                      MEDLINE=21534947; PubMed=11677608;
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87.5%;
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1; Mismatches
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No. 1e+02;
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S., Layman
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Blum H., Bauersachs S., Mewes
Submitted (JAN-2000) to the E
EMBL; ALI37464; CAB70751.1; -
Hypothetical protein.
NON TER 1
SEQUENCE 190 AA; 21833 MW;
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Watanabe K., Kumagai A.,
Suzuki Y., Obayashi M., N.
Nakamura Y., Isogai T., Si
"NEDO human cDNA sequencii
Submitted (AUG-2000) to tl
                                                                                                                                                                                                                                                                                                                    EMBL; AKO26333; BAB15451.1; -.
EMBL; BC020601; AAH20601.1; -.
Hypothetical protein.
SEQUENCE 183 AA: ^^^~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9H616;
Q9H616;
01-MAR-2001
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01-OCT-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein FLJ22680.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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Submitted
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                                                                                       NCBI_
                                                                                                                                Hypothetical p
DKFZP434E1722
                                                                                                                                                                                          Q9NT91
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                                                                                                                       Homo sapiens
                                                                                                                                                                                Q9NT91;
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                           TISSUE=Testis;
                                                                    EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                protein.
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000) to the EMBL/GenBank/DDBJ
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T., Sugano
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Primates;
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54.5%;
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Nishi T., Shibahara T., Tanaka
  W.
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                                        es H.W., Gassenhuber J., Wiemann EMBL/GenBank/DDBJ databases.
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4; Mismatches
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                                                                                                   Craniata; Vo
Catarrhini;
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  D9C9D7BCDE006CE9 CRC64
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01-OCT-2001 (TremBirel. 18, L
01-MAR-2003 (TremBirel. 23, L
Hypothetical protein TV0105.
TV0105 OR TVG0110910.
Trermoplasma volcanium.
"Genome sequence of pathogen.";
Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                               Q8DVU3;
Q8DVU3;
01-MAR-2003
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MEDILINE=20570466; PubMed=11121031;

Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

Kawashima T., Watanabe K., Yamazaki M., Kanehori K., Kav

Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Suzuki M.;

"Archaeal adaptation to higher temperatures revealed by genon

sequence of Thermoplasma volcanium.";

Proc. Natl Acad. Sci. U.S.A. 97:14257-14262(2000).

EMBL; AP000991; BAB59247.1;

TITENORY TERRORS STREET
                                    SEQUENCE FROM N.A.

STRAIN-UAN159 / ATCC 700610 / Serotype C;

MEDLINE=22295063; PubMed=12397186;

MEDLINE=22295063; PubMed=12397186;

Ajdic D., McShan W.M., McLaughlin R.B., Savic G., Chang J.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,

Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti

"Genome sequence of Streptococcus mutans UA159, a cariogenic (
                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003
01-MAR-2003
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Pfam; PF01867; DUF48; 1.

ProDom; PD008695; DUF48; 1.

TIGREPAMS; TIGR00287; TIGR00287;

Hypothetical protein; Complete F
SEQUENCE 322 AA; 37255 MW;
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                                                                                                                                                                                                                                                                                     Streptococcus mutans. Bacteria; Firmicutes;
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       Acad. Sci.
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54.5%;
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Pred. No. 28;
5; Mismatches
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5FB6133DABE746C8 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up)
01-OCT-2002 (TrEMBLrel. 22; Last annotation)
Hypothetical protein FLJ20035.
Homo sapiens (Human).
                                                                                                                                                                                                          Q8IY21 PRELIMINARY; PRT; 1712 AA.
Q16MY21;
Q16MY21;
Q16MY21;
Q16MY21;
Q16MY21;
Q176MBLrel. 23, Created)
Q16MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q16MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ20035.
Homo sapiens (Human).
                                                                                                        Submitted (SEP-2002) to the EMBL; BC038115; AAH38115.1;
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 391 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawabata A., Hikiji T., Kobatake N., Ina Okitani R., Ota T., Suzuki Y., Obayashi Tanaka T., Nakamura Y., Isogai T., Sugar "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBan)
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Hypothetical protein; Complete
SEQUENCE 387 AA; 45217 MW;
                                                                                 Hypothetical
SEQUENCE 17
                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                             NCBI_TaxID=9606;
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6; Conserv
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7; Conserve
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RVSLTAYAMDY 11
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                                                                                 al protein.
1712 AA;
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387 AA; 45217 MW;
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EMBL/GenBank/DDBJ
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Pred. No. 35;
4; Mismatches
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                                                Score 37;
Pred. No.
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46F6D2F75FE69CE0
                                     Mismatches
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                                                                                 E51D3588135D2066 CRC64;
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ayashi M., Nishi
Sugano S.;
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Nishi T., Shib
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Best Local
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01-DEC-2001
01-DEC-2001
01-MAR-2003
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01-MAR-2003
01-MAR-2003
                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-JCM 10545 / 7;

PubMed=1157479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Kosugi H., Takamiya M., Kato Y.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;
                                                                          DNA Res. 8:123-140(2001).
EMBL; AP000985; BAB66235.1;
InterPro; IPR006638; Elp3.
SMART; SM00729; Elp3; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Gmplete proteome.
SEQUENCE 275 AA; 32042 MW; 869625BD4F2C3027 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Vibrio vulnificus CMCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE016801; AA009840.1; -
                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein ST1194.
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Chey H.E.;
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Vibrionaceae; Vibrio.
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Trenarchaeon, Sulfolobus tokodaii strain7.";
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Pred. No.
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                                     Score 36; DB Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8ACAB07128790F68 CRC64;
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Q8PKD3
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Q9Q8H7;
01-MAY-2000
01-MAY-2000
01-DEC-2001
        MEDLINE=22022145; PubMed=12024217;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Quaggio R.B., Contino Vitorello C.B., Camargo L.E.A.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Clearelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Chinal J. E. T., Franco M. T. M., Sena J.A.D., Silva C., de Souza R.F.,
                                                                                                                                                                                                                                xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF1
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Lauganne;
MEDLINE=20032073; PubMed=10562494;
MEDLINE=20032073; PubMed=10562494;
Cameron C., Hota-Mitchell S.; Chen L., Barret
Macaulay C., Willer D., Evans D., McFadden G.
Macaulay C., Willer D., Evans D., McFadden G.
"The complete DNA sequence of myxoma virus.";
                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myxoma virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA
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AA; 32627 M
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Q9EWT9;
Q9EWT9;
Q1-MAR-2001 (TrEMBLrel. 10
01-MAR-2001 (TrEMBLrel. 11
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Taking M.A., Rutherford K., Rutter S.,
Taylor K.,
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STRAIN=A3(2);
STRAIN=BDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., (Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids" and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids" and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids" and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids" and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of ordered cosmids" and "A set of 
"Complete genome sequence of t coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939106; CAC14934.1; -.
HSSP; P41140; 2SFA.
                                                                                                                  STRALE-Steger K.J., har-Seeger K.J., har-
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InterPro; IPR002052; N6 Mtase.
InterPro; IPR000051; SAM bind.
PRINTS; PR00507; N12N6MTFRASE.
PROSITE; PS00092; N6_MTASE; 1.
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Parkhill J., Barrell
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Streptomycineae; Streptomycetaceae; Streptomyces.
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EMBL; AE011861; AAM37095.1;
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e EMBL/GenBank/DDBJ databases
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101-JUN-2001 (TrEMBLrel. 17, L
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SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

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InterPro; IPR001316; EndoptdseSSA.
InterPro; IPR001254; Ser_protease_T
Pfam; PF02983; AL protease; 1.
Pfam; PF000889; trypsin; 1.
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Eukaryota; Metazoa; Chordata; Urochordata;
Stolidobranchia; Styelldae; Polyandrocarpa
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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PA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
PA Generation and initial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004567; PanK_eukar.
Pfam; PF03630; Fumble; I.
Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis.
SEQUENCE 370 AA; 41094 MW; 71EEFA56079F352D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932;
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CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
phosphopantothenate.

ENZYME REGULATION: Regulated by feedback inhibition by CoA and it
thioesters (By similarity).

PATHMAY: Coenzyme A (CoA) biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).

TISSUE SPECIFICITY: Highly expressed in the liver.
SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
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SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
MEDLINE=20512592; PubMed=11058132;
MEDLINE=20512592; PubMed=1 1058132;
MEDLINE=20512592; PubMed=1 N., Agasawara N., Nakasone K., Takaki Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALR_BACHD
Q9KFF9;
use by non-profit institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an or send an email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (See https://or.send.an.email - license agreement (S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics.Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                    This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo the European Bioinformatics Institute. use by non-profit institutions as lo
                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilinucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alanine racemase
ALR OR BH0520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
28-FEB-2003
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-!- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
                                                                                                                                                                                                                                                                                     <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=86665;
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                                                                                                                                                                                                                                                   biosynthesis (By similarity).
CATALYTIC ACTIVITY: L-alanine = D-alanine.
COFACTOR: Pyridoxal phosphate (By similarity)
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PATHWAY: Coenzyme A (COA) biosynthesis; first step.

SUBCELLULAR LOCATION: Cytoplasmic (Probable).

SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE
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ENZYME REGULATION: Regulated by
                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                                                                                                                    FUNCTION: Provides the D-alanine required
                                                                                                                                                                                                                                      PATHWAY:
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updatemase (EC 5.1.1.1).
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Kinase; ATP-binding; Coenzyme A biosynthesis.
70 AA; 41120 MW; 61D982A619E83A78 CRC64;
                                                                                                                                                                                                                                      D-alanine
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                                                                                                              entry is copyright. It is produced through iss Institute of Bioinformatics and the E
                                                                                                                                                                                     Belongs to the alanine racemase family.
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                        noved. Usage by and fo
(See http://www.isb-sib
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                                                                                                                                                                                                                                         biosynthesis;
                                                                                             restrictions
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SEQUENCE
                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                         component of the prespliceosome.";
Proc. Natl. Acad. Sci. U.S.A. 90:6771-6775(1993).
-!- SIMILARITY: Contains 1 Rho-GAP domain.
                                                                                                                                                                                                                                                                                     Purnelle B., Coster F., Goffeau A.;
"The sequence of a 36 kb segment on the left a
X identifies 24 open reading frames including
CDC6, CRY2, the gene for S24, a homologue to the
and two homologues to chromosome III genes.",
Yeast 10:1235-1249(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 68.5 kDa protein in PRP21-UBP12
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PIR; H
H9SP;
           EMBL; X77688; CAA54756.1; -. EMBL; Z49476; CAA89496.1; -. EMBL; L07744; AAB09602.1; -.
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Eukarvota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                   Arenas J.E., Abelson J.N.;
"The Saccharomyces cerevisiae PRP21
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Pfam; PF01168; Ala_racemase N; 1.
PRINTS; PR00992; Ala_RACEMASE.
TIGRPAMs; TIGR00492; alr; 1.
                                                                                                                                                                                                                                            MEDLINE=93342071; PubMed=8341697;
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HAMAP; MF_01201; -; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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388 AA;
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No.
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Best Local S
Matches 6
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P28036;
01-AUG-1992
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-!- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: -!- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: -!- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an reduced acceptor
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         SMART; SM00564; PQQ; 3. IA.
PROSITE; PS00363; BACTERIAL PQQ 1; 1.
PROSITE; PS00364; BACTERIAL PQQ 2; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
Oxidoreductase; PQQ; Heme; Periplasmi
                                                                            InterPro; IPR001479; Bac_PQQ.
InterPro; IPR002372; Bac_PQQ_rep
InterPro; IPR000345; CytC heme b
Pfam; PP01011; Bacterial PQQ; 3.
                                                                                                                                                      EMBL; D00635; BAA00528.1;
PIR; S14270; S14270.
                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                     reduced acceptor.
-i- COFACTOR: PQQ AND HEME.
-i- SUBUNIT: HETEROTETRANER (DEHYDROGENASE, C.)
-smaller unknown subunits) that forms the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acetobacter polyoxogenes. Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23,
01-AUG-1992 (Rel. 23,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. DOMAIN 181 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000198; RhoGAP. SMART; SM00324; RhoGAP; 1. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD; S0003737; ECM25.
GO; GO:0007047; P:cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRÓSITE; PS50238; RHOGAP; 1.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91159482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetobacteraceae; Acetobacter
                                                                                                                                                                                                                                                                                                             COMPLEX.

SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING SPACE (POTENTIAL).

SIMILARITY: BELONGS TO THE BACTERIAL POO DEISMILARITY: Contains 1 cytochrome c domain.
                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                          Q9Z4J7; 1FLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RISLNVYLYDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=2001402;
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54.5%;
             Heme; Periplasmic; Membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
[acceptor] precursor (EC 1.1.99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organization and biogenesis; IMP
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Pred. No.
                                                                                                _repeat.
me_bind.
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POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                         CYTOCHROME, AND TWO
E ALCOHOL DEHYDROGENASE
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                                                                                                                                                                                                                                                                                                                                                             PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two subunits of polyoxogenes.";
                                                                                                                                                                                                                                                         restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                            EMBL; X82894; CAA58066.1; -.
EMBL; Y09480; CAA70688.1; -.
HSSP; O9Z4J7; IFLG:
InterPro; IPR001479; Bac PQQ. repeat.
InterPro; IPR002372; Bac PQQ_repeat.
InterPro; IPR003345; CyCC heme_bind.
Pfam; PF01011; Bacterial PQQ; 3.
SMART; SM00564; PQQ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q44002; 007952;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alcohol dehydrogenase [acceptor] precursor (EC 1.1.99.8).
         DOMAIN
BINDING
BINDING
METAL
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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METAL
                                                                                          PROSITE; PS00363; BACTERIAL PQQ_1; 1.
PROSITE; PS00364; BACTERIAL PQQ_2; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acetobacter europaeus.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
ACBI_TaxID=33995;
                                                                                                                                                                                                                                     entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             SPACE (POTENTIAL).

-i- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DE-
-i- SIMILARITY: Contains.1 cytochrome c domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-DES11 / DSM 6160;
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SEQUENCE
                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thurner C.A.K.;
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7; Conserv
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738 AA;
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                                                                               PQQ;
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                                                                                Heme;
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70.0%;
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 ¥
                                                                               Periplasmic; Membrane; Signal
       ALCOHOL DEHYDROGENASE (ACCEPTOR).
CYTOCHROME C-LIKE.
HEME (COVALENT) (BY SIMILARITY).
HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
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HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LICAND) (BY SIMILARITY);
1E2B6ED7BCD92AF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
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                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduced acceptor.
-!- COFACTOR: PQQ AND HEME.
-!- SUBUNIT: TETRAMER OF NON IDENTICAL CHAINS (DEHYDROGENASE,
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SUBCELLULAR LOCATION: Periplasmic PQQ DEHYDROGENASE FAMILY.
-!- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
-!- SIMILARITY: Contains 1 cytochrome c domain.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACEAC
                                                                                                                                                    PROSITE; PS00363; BACTERIAL PQQ_1; 1.
PROSITE; PS00364; BACTERIAL PQQ_2; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                 InterPro; IPR001479; Bac_PQQ.
InterPro; IPR0002372; Bac_PQQ.
InterPro; IPR000145; CyrC heme refam; PF01011; Bacterial FQQ; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cozier G.E., Giles I.G., Anthony C.;
"The structure of the quinoprotein alcohol dehydrogenase of Acetobacter aceti modelled on that of methanol dehydrogenase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 36-50. MEDLINE=89255070; PubMed=2722742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acetobacteraceae;
NCBI_TaxID=435;
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                                                                                                     SIGNAL
                                                                                                                                                                                                                             SMART; SM00564; PQQ;
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HSSP; Q9Z4J7; 1FLG.
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D90004; BAA14058.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and sequencing of the gene dehydrogenase subunit of alcohol del
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yano K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 171:3115-3122(1989).
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                                                                                                                       PQQ;
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70.0%;
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                                                                                                                            Periplasmic; Membrane; Signal
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Pred. No.
                            ALCOHOL DEHYDROGENASE [ACCEPTOR].
CYTOCHROME C-LIKE.
BASE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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  (See http://www.isb-sib.ch/announce/
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Best Local S
Matches 7
DOMAIN
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                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35,
28-FEB-2003 (Rel. 41,
Alcohol dehydrogenase
subunit I).
                                                                                                                       InterPro; IPR001479; Bac_PQQ repeat. InterPro; IPR002372; Bac_PQQ repeat. InterPro; IPR000345; CytC_heme_bind. Pfam; PF01011; Bacterial_PQQ; 4.
SMART; SM00564; PQQ; 6.
                                                                                                                                                                                     EMBL; D86375;
HSSP; Q9Z4J7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of the genes encoding the three-component bound alcohol dehydrogenase from Gluconobacter suboxydans are expression in Acetobacter pasteurianus.";
Appl. Environ. Microbiol. 63:1131-1138(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gluconobacter oxydans (Gluconobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   005542;
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SIGNAL
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MEDLINE=97208225; PubMed=9055427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetobacteraceae; Gluconobacter
                                       CHAIN
                                                                                                  PROSITE;
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                                                                                                                                                                                                                                                                                                                      SPACE (POTENTIAL).
SIMILARITY: BELONGS TO
SIMILARITY: Contains 1
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                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
CATALYTIC ACTIVITY: A primary alcohol +
                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MEMBRANE-BOUND,
                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: PQQ AND HEME
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                                                                                   PS00363; BACTERIAL PQQ 1; 1.
PS00364; BACTERIAL PQQ 2; 1.
PS00190; CYTOCHROME_C; 1.
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742
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
ydrogenase [acceptor] precursor (EC
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IRON
  ALCOHOL DEHYDROGENASE [ACCEPTOR].
CYTOCHROME C-LIKE.
PYRROLIDOME CARBOXYLIC ACID.
BASE (POTENTIAL).
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RON (HEME AXIAL LIGAND) (BY SIMILARITY).

9C6C9268DABB825A CRC64;
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(See http://www.isb-sib.ch/announce/
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                                                                         Membrane;
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SEQUENCE
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                                                                                                                                                                                                                                                 Haenzelmann P., Dobbek H., Gremer L., Huber R., Meyer O.; "The effect of intracellular molybdenum in Hydrogenophaga pseudoflar on the crystallographic structure of the seleno-molybdo-iron-sulfur flavoenzyme carbon monoxide dehydrogenase."; J. Mol. Biol. 301:1221-1235(2000).
                                                                                                                                                                                                                                                                                                                                                carboxydotrophic Arch. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comamonadaceae; Hydrogenophaga.
NCBI TaxID=47421;
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                            Meyer O., Gremer L., Ferner R., Fe Meyer-Klaucke W., Huber R.; "The role of Se, Mo and Fe in the
                                                                                                                                                                                                                                                                                                                                                           Kraut M., Hugendieck I., Herwig S "Homology and distribution of CO carboxydotrophic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    monoxide dehydrogenase and localization adenine dinucleotide, and iron sulfur Hydrogenophaga pseudoflava.";
J. Bacteriol. 181:5581-5590(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99412255; P
Kang B.S., Kim Y.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dehydrogenase subunit L)
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                                                                                                                                                       Biol.
                                                                                                                                                                 monoxide dehydrogenase."
                                                                                                                                                                                                 MEDLINE=20525277; PubMed=11076018;
Meyer O., Gremer L., Ferner R., Ferner M., Dobbek H.,
                                                                                                                                                                                                                                                                                                              MEDLINE=20425113;
                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90055678; PubMed=2818128;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrogenophaga pseudoflava (Pseudomonas carboxydoflava)
                                                        COFACTOR: Molybdenum (molybdopterin).
SUBUNIT: COMPOSED OF 2 HETEROTRIMERS.
OF A LARGE, A MEDIUM AND A SMALL SUBUD
DIMERIZE TO FORM A HEXAMER.
                                                                                                                   CATALYTIC ACTIVITY:
                                                                                                                                          FUNCTION:
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V: Catalyzes the c
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                                                                      A SMALL SUBUNIT.
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(COVALENT) (BY SIMII
(HEME AXIAL LIGAND)
                                                                                                                                                                               structure
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SIGNAL
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical lipoprotein yfhm precursor.
YFHM OR B2520.
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteria; Gammaproteobacteria; Enterobacteriales;
NCBI_TaxID=562;
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                                                                                     SEQUENCE
                                                                                                                                                                                                            Hypothetical protein; Membrane;
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STRAIN=K12 / MG1655;
STRAINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02738; Ald_Xan_dh_C2; 1.
Pfam; PF0315; Ald_Xan_dh_C; 1.
Oxidoreductase; Molybdenum; Selenium; Selenocysteine; 3D-structure.
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PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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N-ACYL DIGLYCERIDE (POTENTIAL)
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YAJF ECOLI STANDARD; PRT; 302 AA
P23317; P71316; P75705;
01-MAR-1992 (Rel. 21, Created)
01-UN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Hypothetical protein yajf. ...
YAJF OR B0394.
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STRAIN-K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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EMBL; A2000145; AAC73497.1; ALT
EMBL; U73857; AAB18118.1; ALT_IN
EMBL; W64787; AAB23475.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lin D., Namath A., Oefner P., Roberts D., Schramm S., I Submitted (NOV-1996) to the EMBL/GenBank/DDBJ database
                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mapping, sequence, and apparent lack of function of ar
the Escherichia coli arabinose regulon.";
J. Bacteriol. 173.765-7771(1991)
-!- SIMILARITY: BELONGS TO THE ROK (NAGC/XYLR) FAMILY.
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Submitted (DEC-1993)
                                                                                   Hypothetical SEQUENCE 30
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EcoGene; EG11288; yajF
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nce 277:1453-1474(1997).
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302 AA; 32500 MW; 9791F9C29C91049C CRC64;
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                                RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Komno H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Hayashizaki Y.,
A Hayashizaki Y.,
TISSUE-Liver, and Skeletal muscle;

X MEDLINE-22388257; pubMed=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max, Rubin G.M., Hong L.,

X ALL C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X ALL C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X ALL C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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X ALL C., Marusina K., Farmer A.A., Rubin G.M., Wallahy S.J.,

X ALL C., Walek J.A., Gunaratne P.H.,

X ALL C., Marusina K.J., Malek J.A., Gunaratne P.H.,

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QBK4K6; Q9D3K1;
28-FEB-2003 (Rel
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[1]
SEQUENCE FROM N.A. (ISOFORM 2), AND MEDLINE=20092916; PubMed=10625688; Rock C.O., Calder R.B., Karim M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The murine pantothenate differentially regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2],
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1), CHARACTERIZATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22090536; PubMe
Rock C.O., Karim M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANK1 OR PANK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409:685-690(2001).
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M.A., Zhang Y.M., Jackowski
thenate kinase (Pank1) gene
gulated pantothenate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISOFORM 2).
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O.F
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gulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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intracellular
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                                                        S.W.
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PNK2_HUMAN ST ID PNK2_HUMAN ST AC Q9BZZ3; Q8N7Q4; Q DT 28-FEB-2003 (Rel. DT 28-FEB-2003 (Rel.

STANDARD; PRT; 57
7Q4; Q8TCR5; Q9BYW5; Q9HAF2; (Rel. 41, Created) (Rel. 41, Last sequence upd

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Last sequence update)

RESULT 13

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Best Local S
Matches 6
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fahey J., Helton E., Ketteman M., Madan A., Rodrigues Whiting M., Madan A., Young A.C., Shevchenko Y., Bouth Blakesley R.W., Touchman J.W., Green E.D., Dickson M. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 human and mouse cDNA sequences.";
                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                           MGD;
                                                                                                                                                                                                                                                                                         EMBL; AF200357; AAF23952.1;
EMBL; AF347700; AAM77216.1;
EMBL; AK017345; BAB30700.1;
EMBL; BC023496; AAH23496.1;
                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
i- FUNCTION: Plays a role in the physiological regintracellular COA concentration.
-i- CATALYTIC ACTIVITY: ATP + pantothenate = ADP +
                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                 Alternative splicing
                                                                                                                                                                                                                                Ptam;
                                                                                                                                                                                                              Transferase; Kinase; ATP-binding; Coenzyme
                                                                                                                                                                                                                                             nterPro;
                                                                                                                                                                                                                                        GO:0004594; F:pantothenate kinase activity; IDA erpro; IPR004567; Pank_eukar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=1; Synonyms=PanK1-alpha;
IsoId=Q8K4K6-1; Sequence=Displayed;
Name=2; Synonyms=PanK1-betta;
IsoId=Q8K4K6-2; Sequence=VSP 004522,
TISOID SPECIFICITY: Expressed in liver
highly expressed in heart and skeletal
is expressed exclusively in testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulatory domain.
SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: The N-terminal extension, present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by acetyl-CoA and malonyl-CoA.
PATHWAY: Coenzyme A (CoA) biosynthesis;
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thioesters. Strongly inhibited by acetyl-CoA and by manyl-CoA and also inhibited by high concentration of non-esterified CoA (CoASH). Isoform 1 is inhibited by high concentration of non-esterified CoA (CoASH) and strongly inhibited by acetyl-CoA and by malonyl-CoA. Isoform 2 is stimulated by CoA and weakly inhibited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphopantothenate.
ENZYME REGULATION: Regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
506
                                                                                                                                                                                                                                                                           MGI:1922985; Pank1
                                                                                                                                                                                                                                 PF03630;
                                                           Similarity 6; Conserv
MKLLAYAMDF
                            VSLTAYAMDY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helton E., Ketteman M.,
                                                                                                                        548 AA;
                                                                                                                                                      176
                                                            Conservative
                                                                                                                                                                                                                                Fumble;
                                                                                                                                                      185
515
                                                                                                                                                                                     175
                                                                                                                        60091 MW;
                                                                        60.0%;
                                                           Score 33; DB Pred. No. 46; 2; Mismatches
                                                                                                                                                   /FTId=VSP_004522
MDSGRKNRPP -> MK
                                                                                                                        /FTId=VSP_004523.
C916709D048E429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            feedback inhibition
                                                                                                                                                                                     (in isoform
                                                                                                                                                      -> MKLVNGRKQT (in
                                                                                                                                                                                                                                                                                                                                                                                                                  as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSP_004523;
and_kidney. Isoform
muscle, whereas iso
                                                                                                                                                                                                                A biosynthesis;
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                                                                                        Length 548;
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1 G.G.,
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RRRRRRRRR RROCCO GREET

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Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beard D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
R. Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
R. Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
R. Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
R. Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
R. Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
R. Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
R. Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
R. Hammond S., Harley J.L., Heath P.D., Ho.S., Holden J.L., Howden P.J.,
R. Hammond S., Harley J.L., Heath P.D., Ho.S., Holden J.L., Howden P.J.,
R. Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
R. Kimberley J.L., Heath P.D., Ho.S., Holden J.L., Howlor S.,
R. A. Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
R. A. Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
R. Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
R. A. Milne S.A., Nistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
R. A. Philliames A., Patel R., Pearce T.A.V., Peck A.I.,
R. A. Philliams S.A., Patel R., Soderlund C., Steward C.A., Sulston J.E.,
R. A. Swann R.M., Sycamore N., Taylor R., Teee L., Thomas D.W., Thorpe A.,
R. A. Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
R. A. Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,
R. A. Whitehead S.L., Whittaker P., Willey D.L., Beck S.,
R. A. Milne S.J., Markey D.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                            Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima N., Ishi S., Yamamoto J., Irie R., Otsuki T., Sato H., Wakamate Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishil A. Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., A. Kikuchi H., Kanada K., Wagatsuma M., Murakawa K., Kanehori K., A. Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Ota T., A. Hayashi K., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., A. Hara R., Takeuchi K., Arita M., Nabekura T., Kawai Y.;

"NEDO human cDNA sequencing project.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Testis;
Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., S
Natsumoro K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataok
Kaeriyama S., Satoh I., Kamata K., Takami S., Terask
Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terask
Kuga N., Kuroda A., Satoh I., Kamata K., Sato H., Wak
DISEASE.
MEDLINE=22053542; PubMed=12058097; Ching K.H.L., Westaway S.K., Gitsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The DNA sequence and com
Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rogers
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Hum. Mol. Genet. 12:321-327(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoertnagel K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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(Pantothenic
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                                                                                                                                                 (MAR-2002)
                                                                                                                                                                               Beyer
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                                                                                                                                                                                                                                                    406-570
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cient in pantothenate kinase-associated
                                                                                                                                              H.-W., Weil B., W:
EMBL/GenBank/DDBJ
Gitschier J., Higgins J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND VARIANT
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                                                                                                                                          Wiemann S.;
BJ databases
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Terashima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiohata
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EMBL; EMBL;

ALT_INIT.

Genew;

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CC -:- TISSUE SPECIFICITY: Ubiquitous.

CC -:- DISEASE: Defects in PANK2 are the cause of pantothenate kinase-
CC -:- DISEASE: Defects in PANK2 are the cause of pantothenate kinase-
CC associated neurodegeneration (PKAN) (MIM:234200], formerly known
CC as Hallervorden-Spatz syndrome (HSS). PKAN is an autosomal
CC recessive neurodegenerative disorder associated with iron
CC commulation in the brain. Clinical features include
CC extrapyramidal dysfunction, and a relentlessly progressive course.
CC Atypical PKAN is diagnosed in individuals who may not fit with the
CC diagnostic criteria of PKAN yet have radiographic or pathologic
CC evidence of increased basal ganglia iron.
CC evidence of increased basal ganglia iron.
CC IDISEASE: Defects in PANK2 are the cause of
CC and pallidal degeneration (HARP) [MIM:607236]. HARP is a rare
CC syndrome with many clinical similarities to PKAN.
CC -- MISCELLANEOUS: The HSS syndrome has been proposed to be renamed to
CC PKAN because of the unethical activities of Julius Hallervorden
EMBL;
EMBL;
EMBL;
                                                                                                                                                           between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurology
[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21372465; PubMed=11479594; Zhou B., Westaway S.K., Levinson B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO-413; AS:
SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS GLN-111 AND GLY-126, VARIANTS PKAN VAL-219; ALA-234; TRP-264; CYS-278; VAL-282; CYS-286; ILE-327; PRO-351; SER-355; ILE-404; PRO-413; ASN-471; THR-497; ILE-500; ARG-521 AND MET-528, AND TISSUE
                                                                                                                                                 entities requires a
                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hallervorden-Spatz syndrome.
Nat. Genet. 28:345-349(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayflick S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: Maybe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurodegeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayflick S
                                                                                                                                  send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel pantothenate kinase
                                                                                                                                                                                                                                                                       gene model prediction. CAUTION: In addition to the presence of position 124, it is not excluded that the
                                                                                                                                                                                                                                                                                                                   PKAN because of the unethical activities and Hugo Spatz during World War II.
SIMILARITY: BELONGS TO THE EUKARYOTIC PAN
CAUTION: Ref. 2 sequence differs from that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Coenzyme A (CoA) biosynthesis; SUBCELLULAR LOCATION: Cytoplasmic and mi ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative initiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thioesters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
         ; AF494409; AAN32907.1;
AL353194; CAC15924.2;
AL031670; CAC32829.1;
AK021791; BAB13897.1;
AK021791; BAC05173.1;
AK07796; BAC05173.1;
AL713654; CAD28463.1;
HGNC:15894; PANKZ.
                                                                                                                                                                                                                                                         exceptionally also serve as an alternative initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative
                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9BZ23-1; Sequence=Displayed
Note=Mitochondrial isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comment=2 isoforms, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9BZ23-2;
                                                                                                                                  an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58:1673-1674 (2002)
                                                                                                                                   email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is allelic with
                                                                                                                                s a license agreement
to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the master regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence=VSP_007424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP +
                                                                                    ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (shown here)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PANK2) is
                                                                                                                                   .ch) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             feedback inhibition
                                                                                                                                                                                                                                                                          that the
                                                                                                                                                 (See http://www.isb-sib.
                                                                                                                                                                            There are no rest
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                                                                                                                                                                                                                                                                                                                      that
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                                                                                                                                                                                                                                                                                                                     PANTOTHENATE KINASE FAMILY
                                                                                                                                                                                                                                                                                       ุ่ม
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RESULT 14
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15-SEP-2003 (Rel. 42, Last annotation update)
Pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Clatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.J., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Botherch A., Schein J.E., Jones S.J.M., Wyers R.M., "Generation and initial analysis of more than 15,000 full-length numan and mouse cDNA sequences.";
RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                           This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished observations (JUL-2001).
i- FUNCTION: Plays a role in the physiological regulation intracellular COA concentration (By similarity).
-i- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
                                                                            between
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Hayflick S.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                   IsoId=Q8TE04-3; Sequence=VSP_004520, VSP_004521; TISSUE SPECIFICITY: Expressed in liver and kidney.

DOMAIN: The N-terminal extension, present in isoform 1 may be the
                                                                                                                                                                                                                                                                                                                                      PATHWAY: Coenzyme A (COA) biosynthesis; first SUBCELLULAR LOCATION: Cytoplasmic (Probable). ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3; Name=1; Synonyms=PanKl-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphopantothenate.

phosphopantothenate.

ENZYME REGULATION: Regulated by feedback inhibition by CoA and its thioesters. Strongly inhibited by acetyl-CoA and by manyl-CoA and thioesters. Strongly inhibited by acetyl-CoA and by manyl-CoA and thioesters.
                                                                                                                            regulatory domain.

SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.

CAUTION: Isoform 2, although confirmed in the murine ortholog, is

only partially cloned and needs a further complete identification.
                                                                                                                                                                                                                                                                 Name=3
                                                                                                                                                                                                                                                                                                    Name=2
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                                 SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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6; PubMed=11809413;
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Frong H., Jiang M., Ying K., Xie.
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S.K., Levinson
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               A KEDLINE-98044033; PubMed-9384377;

X KINST F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

A Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

A Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

A Glims Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Hibert H., Holsappel S., Koningstein G., Krogh S., Kumano M.,

Kan Akobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

Kurita K., Lapidus A., Lardinois S., Laber J., Lazarevic V.,
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Transferase; Kinase; ATP-binding;
Alternative splicing.
VARSEPLIC 1 235 MIXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
Bacteria; Firmicutes;
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A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
A Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
A Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
A Sorokin M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandambol M., Vannier F., Vassarotti A.,
A Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
A Winters P., Wipat A., Yamamotto H., Yamane K., Yasumotto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
                                         Query Match
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Matches 6
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PIR; D0917; D0917.

Subtilist; BG1253; dnaE.

InterPro; IPR004013; PHP C.

InterPro; IPR004105; POIC alpha.

InterPro; IPR004365; tRNA anti.

InterPro; IPR004365; tRNA anti.

Pfam; PF02811; PHP C; 1.

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EMBL; Z99118; CAB14883.1;
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME RESPONSIBLE FOR MOST OF THE REPLICANTURE SYNTHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITES 3' TO 5' EXONUCLEASE ACTIVITY. THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY). CATALLYIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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A;Accession: \$26315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <STA>
A;Cross-references: EMBL:X59208; NID:g52079; PIDN:CAA41918.1; PID:g1334042
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;2-85/Domain: immunoglobulin homology <IMM>

R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino A;Reference number: S26309; MUID:91341421; PMID:1908510

acid interchange in a protein

20-Jun-2000

Ig heavy chain V region - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C;Accession: S26315

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ALIGNMENTS

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, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC0823
                                                                                                                                                                                                                                                                                                                                            probable lipoprotein STY2778 [imported] - Salmonella enterica subsp. enterica serovar TyC;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AC0823
                                                                                             A;Molecule type: DNA
A;Residues: 1-1644 <PAR>
A;Cross-references: GB;AL513382; PIDN:CAD02735.1;
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                                                               A;Gene: STY2778
                                                                                                                                                                                                                                                                                                      R;Parkhill, J.; Dougan, G.; James, K.D.; th, T.; Connerton, P.; Cronin, A.; Davis,
                                                                                                                                                              A; Status: preliminary
  Query Match
Best Local Similarity
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Best Local
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  69.1%;
87.5%;
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100.0%; Pred. No.
tive 0; Mismatch
    Score
Pred.
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    38;
                                                                                                                                                                                                                                                                                                        Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
DB
30;
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                                                                                                     PID:g16503746; GSPDB:GN00176
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                       Length 1644
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Salmonella enterica
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conserved hypothetical exported protein SMb20724 [imported] - Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: G96020 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herroc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e. A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G96020
A;Status: preliminary
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A; Residues: 1-345 < CLI>
A; Residues: 1-345 < CLI>
A; Residues: GNBL: AL049587; PIDN: CAB40691.1; GSPDB: GN00070; SCOEDB: SC5F2A.24
Perimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, April 1999
A;Reference number: Z21573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable oxidoreductase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 C;Accession: T35266
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C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: T46408
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Best Local
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esidues: 1-190 <AAA>
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Local Similarity 54.5%;
nes 6; Conservarion
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                                                                                                                                                                                                                                                                                                                                                               63.6%;
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Pred. No. 5.4;
4; Mismatches
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Pred. No.
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25;
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                                                             from the N2-fixing end
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H83714
                                          A; Molecule type: DNA
A; Residues: 1-599 < PUR >
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                                                                                A;Status: nucleic
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Best Local
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       Abelson, J.N.
                          EMBL:X77688; NID:g1183992; PIDN:CAA54756.1; PID:g547591
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A;Kotessam...
A;Kotatus; preliminary
A;Molecule type: DNA
A;Residues: 1-388 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04239.1; GSPDB:GN00
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04239.1; GSPDB:GN00
                  N,Alternate names: hypothetical protein J0325
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S46630; S30800; S56988
R;Purnelle, B.; Coster, F.; Goffeau, A.
Yeast 10, 1235-1249, 1994
A;Title: The sequence of a 36 kb segment on the left arm of yeas
ase gene ACO1 and two homologues to chromosome III genes.
A;Reference number: S46621; MUID:95274326; PMID:7754713
A;Accession: S46630
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A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F., L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bacillus halodurans
C;Date: 01-pec-2000 #sequence_revision 01-pec-2000
C;Accession: H83714
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                        hypothetical protein YJL201w - yeast (Saccharomyces cerevisiae) N;Alternate\ names:\ hypothetical\ protein\ J0325
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Similarity 60.0%;
6; Conservative
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acid sequence not shown
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RESULT 9
JS0326
                                                     A;Reference number: JS0326; MUID:89255070; PMID:2722742 A;Accession: JS0326
                                                                                                                                              C;Species: Acetobacter aceti
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C;Accession: JS0326
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R;Tamaki, T.; Fukaya, M.; Takemura, H.; Tayama, K.; Okumura, H.; Kawamura, Y.; Nishiyama Biochim. Biophys. Acta 1088, 292-300, 1991
A;Title: Cloning and sequencing of the gene cluster encoding two subunits of membrane-bc A;Reference number: S14270; MUID:91159482; PMID:2001402
                                                                                                 R;Inoue, T.; Sunagawa, M.; Mori, J. Bacteriol. 171, 3115-3122, 19 A;Title: Cloning and sequencing
                                                                                                                                                                                                    alcohol dehydrogenase (EC 1.1.-.-) 72K chain precursor -
C;Species: Acetobacter aceti
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A;Experimental source: strain NBI1028
C;Complex: heterodimer of 72K and 44K chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alcohol dehydrogenase, membrane-bound (EC 1.1.-.-) 72K chain precursor - Acetobacter C;Species: Acetobacter polyoxogenes A;Variety: strain NBI1028
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A; Residues: 1-599 < PUW>
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                        A; Molecule type: DNA
A; Residues: 1-742 < INO>
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A;Cross-references:
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A;Residues: 1-738 <TAM>
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      Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ywords: alcohol metabolism; membrane protein; oxidoreductase
35/Domain: signal sequence #status predicted <SIG>
-738/Product: alcohol dehydrogenase 72K chain #status predic
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he Saccharomyces cerevisiae PRP21 gene product is required for pre-splid
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GB:D90004; GB:M26951; NID:g216193; PIDN:BAA14058.1; PID:g216194
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Pred. No. 71;
1; Mismatches
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Pred. No.
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R;Hayashi, T.; Makino, N.; Yahara, S.; Shida, A., ..., gasawara, N.; Yasunaga, T.; Kuhara, S.; Shida, A., ..., ....
DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
                                                                                                             A;Access.v....A;Arcess.v...A;Arcess.v...A;Arcess.v...A;Arcess.v...A;Arcess.v...A;Arcess.v...A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1653 <HAY
A;Residues: 1-1653 <HAY
A;Cross-references: GB:BA000007; PIDN:BAB36809.1; PID:g13362856; GSPDB:GN00154
A;Cross-references: GB:BA000007; PIDN:BAB36809.1; PID:g13362856; GSPDB:GN00154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Takemura, H.; Kondo, K.; Horinouchi, S.; Beppu, T.
J. Bacteriol. 175, 6857-6866, 1993
A;Title: Induction by ethanol of alcohol dehydrogenase activity in Acetobacter pasteuria. A;Reference number: A49340; MUID:94042848; PMID:8226628
A;Accession: A49340
                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: B91052
                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein ECs3386 [imported] - Escherichia coli (strain O157:H7, substrain RIC;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:D13893; NID:g517067; PIDN:BAA40252.1; PID:g452586 C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: 'glucose dehydrogenase (pyrroloquinoline-quinone) C;Keywords: alcohol metabolism; NAD; oxidoreductase F;1-35/Domain: signal sequence #status predicted <SIG> F;36-742/Product: alcohol dehydrogenase 72K dehydrogenase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain K6033
A; Note: amino terminal of mature protein is confirmed
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Pred. No. 2e+C
1; Mismatches
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M.; Shinagawa, H.
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1253

LTAYVMDF 1260

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C.G.

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Ig heavy chain (anti-biotin) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S32786
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G65028
A;Residues: 1-118 <BAG>
A;Cross-references: GB:S59639; NID:g299965; PIDN:AAB26438.1; PID:g299966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                        C;Accession: S32786
R;Bagci, H.; Kohen, F.; Kuscuoglu, U.; Bayer, E.A.; Wilchek, M.
FEBS Lett. 322, 47-50, 1993
                                                                                                                                               A; Title: Monoclonal anti-biotin antibodies A; Reference number: S32786; MUID:93245957; A; Accession: S32786
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G65028
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhewiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
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S32786
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A;Residues: 1-1653 <BLAT>
A;Cross-references: GB:AE000338; GB:U00096; NID:gl788862; PIDN:AAC75573.1; PID:gl788868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein b2520 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
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C;Species: Escherichia coli
                                                                                               A; Molecule type: nucleic acid
                                                                                                                        A; Status: preliminary
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;Cross-references: GB:AE005174; NID:g12516921; PIDN:AAG57634.1; GSPDB:GN00145;
;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
Accession: G65028
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Pred. No. 2e+02;
1; Mismatches
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Pred. No. 2e+02;
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Job time : 16.85 secs

Search completed: September 10,

2003, 17:42:42

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R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struces.
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F;15-97/Domain: immunoglobulin homology <IMM>
В
                                                                                                                                                                                                                                                                           A;Reference number: A53285; MUID:92017897; PMID:1922102
A;Accession: B53285
                                                                                                                                                                                                                                                                                                                                                                              C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change C;Accession: B53285
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                              S
                                                                                                                                   F;15-98/Domain:
                                                                                                                                                       C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                    A; Note: sequence inconsistent with nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIN:63295, NCBIP:63300)
                                                                                                                                                                                                                        A; Molecule type: mRNA; protein A; Residues: 1-119 < SAW>
                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Mus musculus (house mouse)
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                                                                    Matches.
                                                                                                                                                                  Superfamily: immunoglobulin V region;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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US-10-156-761-9210
        US-10-238-075-368
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US-09-880-748-231
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Sequence 19, Appl
Sequence 7, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 3288, Ap
Sequence 3288, Ap
Sequence 402, Appli
Sequence 209, Ap
Sequence 2309, Ap
Sequence 999, Ap
Sequence 999, App
Sequence 999, App
Sequence 999, App
Sequence 231, App
Sequence 318, App
Sequence 31, App
Sequence 331, App
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45	44	43	42	41	40	39	38	37	36	35	34		32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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ALIGNMENTS

US-09-759-112A-19

Sequence 19, Application US/09759112A Publication No. US20030100741A1 GENERAL INFORMATION:

APPLICANT: Mueller, APPLICANT: Kohler,

Sybille Heinz

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RESULT 2
US-09-759-112A-7
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                                                       Sequence 7, Application US/09759112A Publication No. US20030100741A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 19
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLECTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE TITLE OF INVENTION: ANTIBODIES FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
APPLICANT: Mueller, APPLICANT: Kohler, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 11
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Sybille
Heinz
NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
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FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 121
TYPE: PRT
ORGANISM: mouse
US-09-759-112A-7
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9210, Application US/10156761 Publication No. US20030119018A1
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Best Local Similarity
                                                                                                                                                                                                                Sequence 5, Application US/09802077 Patent No. US20010033842A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 9210
LENGTH: 339
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                                APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: PO718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
PRIOR APPLICATION NUMBER: US 08/185,899 PRIOR FILING DATE: 1994-01-26
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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Pred. No. 0.0024;
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; SEQ ID NO 5
; LENGTH: 130
; TYPE; PRT
; ORGANISM: Mus musculus
US-09-802-077-5
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PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/U
PRIOR FILING DATE: 1992-08-14
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Matches
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Patent No. US20010038839A1
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Best Local Similarity
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PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
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CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 2001-03-08
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PRIOR APPLICATION NUMBER: US 08/405,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
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75.0%;
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Pred. No.
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Pred. No.
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Sequence 5, Application US/09925179
Publication No. US20030044858A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-1gE Antibodies (as amended)
FILE REFERENCE: P0718P2C1D1C1US
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION TOMBER: US 08/466,163
PRIOR APPLICATION TOMBER: US 08/466,163
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APPLICANT: Presta, Leonard G.
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PRIOR FILING DATE: 1995-03-15

APPLICATION NUMBER: US 08/185,899

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RESULT 8
US-10-128-714-3288
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Best Local Similarity
Marches 6; Conserve
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 249
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                              Sequence 3288, Application US/10128714
Publication No. US20030119013A1
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
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TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES
TITLE OF INVENTION: TO CD38 TO TREAT MULTIPLE MYELOMA
FILE REFERENCE: 150.188US2
CURRENT APPLICATION NUMBER: US/09/730,374
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: PST/US99/12512
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-04
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APPLICANT: Donovan, Kat
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PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
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)S: 68
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75.0%;
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Pred. No.
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Pred. No. 32;
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US-10-128-714-8288
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PRIOR FILLING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILLING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILLING DATE: 2001-06-05
PRIOR PELLORION NUMBER: US 60/303,899
PRIOR PELLORION NUMBER: US 60/303,899
PRIOR PELLORION NUMBER: US 60/303,899
PRIOR PELLORION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/306,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILLING DATE: 2001-08-31
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PRIOR PILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8288
LENGTH: 1199
Type: nom
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Best Local S
Matches 6
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LENGTH: 1046
                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 1018-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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212 MSLTSYSMD
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                                       2 VSLTAYAMD 10
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                                                                                                                                                                                      Aspergillus fumigatus
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Zamudio, Carlos
                                                                                Conservative
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Pred. No.
                                                                              Score 34; DB 15;
Pred. No. 3.5e+02;
3; Mismatches 0
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RESULT 10 US-09-741-669-402

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US-09-925-299-999
; Sequence 999, Application US/09925299
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Best Local Similarity
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                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-880-748-2309
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; SEQ ID NO 402
LENGTH: 1653
TYPE: PRT .
ORGANISM: Escherichia coli
US-09-741-669-402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Oyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for
TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITA, 009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/276,248
RIOR FILING DATE: 2001-03-16
RIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                                                                60.0%;
Local Similarity 55.6%;
les 5; Conservative
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Pred. No. 5.
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Pred. No. 4
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US-09-880-748-231
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US-09-925-299-999
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US-09-925-299-999
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SEQ ID NO 999
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR PELICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
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o. US20030040617A9
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; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-231
                                                                                                                                                                                                                                                                          APPLICANT: IN.S.ER.M.

APPLICANT: IN.S.ER.M.

TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei FILE REFERENCE: BLANDINE

CURRENT APPLICATION NUMBER: US/10/238,075

CURRENT FILING DATE: 2002-09-10

PRIOR APPLICATION NUMBER: 0003145

PRIOR APPLICATION NUMBER: 0003145

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: Patentin version 3.1

SEQ ID NO 368

LENGTH: 329

TYPE: PRT

ORGANISM: Escherichia coli
Search completed: September 10, 2003, 17:50:27 Job time: 23 secs
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US-10-238-075-368
                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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103 TLTSYVLDY 111
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2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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GenCore version (c) 1993 - 2003
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	INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 39 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO	
	DATE: 3-DEC-199 FICATION: FICATION: AGENT INFORMATIO Bucca, Daniel RATION NUMBER: 4 NCE/DOCKET NUMBER NCE/DOCKET NUMBER UNICATION INFORMA ONE: 202-756-8699 X: 202-756-8699	
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                                                                                                                                                                                                 Sequence 5, Application US/08652558 Patent No. 5861155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      ry Match
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REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
COMPUTER READABLE FORM:
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                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                     Local
              COUNTRY: U
                                                                                                                                     TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                      ADDRESSEE:
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                                           MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: protein
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75 STATE STREET, 23RD FLOOR
                                                                        3: BANNER & WITCOFF
75 STATE STREET, 23RD FLOOR
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                                                                                                                                                                    AUGUSTINE YEE-THARN
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72.78;
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Pred. No.
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CENERAL INFORMATION:
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Best Local Similarity 72.7%;
Matches 8; Conservative 1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                    TELEFAX: 617-345-9111 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                           APPLICATION NUMBER: US/08/652,5
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc.
COMPUTER: IBM PC com
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FILLING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: VANCETT: THE PORT OF THE PORT OF THE PORT OF THE PORT OF THE PORT OF THE PORT OF THE PORT OF THE PORT OF THE PORT OF T
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/II
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SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                    NAME: YANKWICH, LEON R. 237
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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STRANDEDNESS: sir
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OPERATING SYSTEM:
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75 STATE STREET, 231
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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M PC compatible
TEM: PC-DOS/MS-DOS
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DN: HUMANIZED ANTIBODIES AND USES
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Pred. No.
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                                                                                                                                                                                                Best Loc
Matches
               Sequence 8, Applicati
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, A
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                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/652,55
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1B94/003.
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
FORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
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TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
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 APPLICANT: LIN, AUG
                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                            Application US/08652558
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AUGUSTINE YEE-THARN
DN: HUMANIZED ANTIBODIES AND USES
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72.7%;
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Pred. No. 0.25;
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Pred. No. 0.
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US-08-652-558-9
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                                  COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, A
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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TELECOMMUNICATION INFORMATION:
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FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/
SOPTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: PCT/IB94/0
FILING DATE: NOVEMBER 21, 1994
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les 8; Conserv
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REGISTRATION NUMBER: 30,237
                                                                                                                                                                                                       ZIP: 02109
                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                  CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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75 STATE STREET, 231
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llarity 72.7%;
Conservative
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IBM PC compatible
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                     PCT/IB94/00387
                                                                                                                                                                                                                                                                                  23RD FLOOR
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Pred. No. 0.25;
1; Mismatches
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TELEPHONE: 617-345-910(
TELEPAX: 617-345-911)
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: line-
MOLECULE TOPOLOGY: line-
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Best Local S
                                                Matches
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APPLICANT: LIN, A
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TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            APPLICATION UNMBER: PCT/IB94/00 FILING DATE: NOVEMBER 21, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMANIZITITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                             Local Similarity hes 8; Conserv
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: JUNE 6
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              RVSLTAYAMDY 11
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DN: HUMANIZED ANTIBODIES AND USES
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72.7%;
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                                                             Score 42; DB 2;
Pred. No. 0.25;
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Pred. No. 0.25;
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RESULT 11
US-09-254-189-4
Sequence 4, Application US/09254189
, Patent No. 6150792
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US-09-254-189-3
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TITLE OF INVENTION: Sequence Listing
Patent No. 6150792
FILE REFERENCE: 3526/00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09254189
Patent No. 6150792
                                                                                                                                                      Best Local Similarity Matches 8; Conserv
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TYPE: PRT
ORGANISM: Artificial Sequence
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72.7%;
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GENERAL INFORMATION:
APPLICANT: Lundquist, Tomas
TITLE OF INVENTION: Sequence Listing
Patent No. 6150792
PILE REFERENCE: 3526/00000
CURRENT APPLICATION NUMBER: US/09/254,189
CURRENT FILING DATE: 1999-03-02
EARLIER APPLICATION NUMBER: 00/000,000
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/254,189
CURRENT FILING DATE: 1999-03-02
EARLIER APPLICATION NUMBER: 00/000,000
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6
                                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence:humanized OTHER INFORMATION: monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:humanized OTHER INFORMATION: monoclonal antibody
                     76.4%; Score 42; DB 3; 72.7%; Pred. No. 0.25;
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Pred. No. 0
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                                           Length 120;
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GENERAL INFORMATION:

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; Sequence 6, Application US/09254189
; Patent No. 6150792
; GENERAL INFORMATION:
APPLICANT: Lundquist, Tomas
; TITLE OF INVENTION: Sequence Listing
Patent No. 6150792
; FILE REFERENCE: 3526/00000
; CURRENT APPLICATION NUMBER: US/09/254,189
; CURRENT FILING DATE: 1999-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATENT OF INVENTION: Sequence Listing
PATENT NO. 6150792
PILE REFERENCE: 3526/00000
CURRENT APPLICATION NUMBER: US/09/254,189
CURRENT FILING DATE: 1999-03-02
FARLIER APPLICATION NUMBER: 00/000,000
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 120
TYPE: PRT
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US-09-254-189-5
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Best Local
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Patent No. 6150792
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LENGTH: 120
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CURRENT APPLICATION NUMBER: US/09/254,189
CURRENT FILING DATE: 1999-03-02
EARLIER APPLICATION NUMBER: 00/000,000
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6
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TITLE OF INVENTION: Sequence Listing
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:humanized
OTHER INFORMATION: monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             st Local Similarity
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72.7%;
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Pred. No. 0.
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Pred. No. 0.25;
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LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Unn-1995
APPLICATION UNMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA: 7.
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAX-1992
PRIOR APPLICATION NUMBER: 07/744768
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVOBOOM, Craig G.
REGISTRATION UNMBER: 39.044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 00/000,000
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                        TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
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OTHER INFORMATION:
                                                                                                                   REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIF: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC COMPATION
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Winpertin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jardieu, Paula M. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/466,151 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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POPOLOGY:
                                 ENGTH:
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Amino Acid
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                                                                                         650/952-9881
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72.7%;
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Pred. No. 0.
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US-08-466-151-5

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US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
PILE REFERENCE: P0718P2C1D1
; URRENT APPLICATION NUMBER: US/08/466,163B
; URRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LEUNGTH: 130
; TYPE: PRT
ORGANISM: Mus musculus
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Search completed: September 10, 2003, 17:43:22 Joh time: 15.95 secs
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US-08-466-163B-5
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                    Query Match 61.8%; Score 34; DB 4; Length 130; Best Local Similarity 75.0%; Pred. No. 12; Matches 6; Conservative 1; Mismatches 1; Indels
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99 VVAYAMDY 106
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Pred. No. 12;
1; Mismatches 1; Indels
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                Score
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seq length: 2000000000
          A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
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55
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Gapop 10.0 , Gapext 0.5
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:
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                        AAO18534
AAY91019
AAO18528
AAY22433
AAY22429
AAY22430
AAY22431
AAY22431
    ABG09046
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AAG21230	AAG54795	AAG21231	AAG21232	ABP46298	AAP40032	AAP80156	AAP80155	AAG98354	АВJ26230	ABJ25630	AAR05235	AAR20192	AAR13993	AAW87786	AAO16379	AAO16375	AAE21711	AAB94366	AAY69523	AAY43867	AAP90542	AAY85196	AAR33308	AAR24562	AAR24561	AAR24560	AAR24558	AAR24557	AAR24556	AAR24555	AAP90540	AAY91067	AAR77303	AAO16433	ABP43853
Zea mays protein f	ÇD.	m	Zea mays protein f	BLys	nt i	Biosynthetic antib	CDRs from				Amino acid sequenc	ADH complex protei	A.altocetigenes me	Fusion protein L49	Murine pantothenat	pantoth	PKIN-6 F	Human protein sequ	CD38 antibod	Heavy chain (VH) g	acid e	chain		x mouse	x mouse	x mouse	x mouse	Human x mouse modi	x mouse	Human x mouse modi		ces no	ā	Ö	FLJ20035 fis clone

ALIGNMENTS

RESULT 1 AAO18534 AAO18534 AAO18534 AAO XX AAC AAO XX AAC AAO AC AAO AC AAO AC AAO AC AAO AC AAO AC AAO AC AAO AC AAO AC AAO AAO	AAO18534 standard; Peptide; 11 AA. AAO18534; 11-OCT-2002 (first entry) Murine Mab 1F7 heavy chain CDR3 region. Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection. Mus sp. W0200255668-A2. 11-JAN-2002; 2002WO-US00927.
X A S	AA018534;
X 3 3	
X H	Murine Mab 1F7 heavy chain CDR3 region.
₹ \$	Mouse; 1F7; antibody; immune modulator; anti-HIV antib
₹.	complementarity determining region; framework-determin
ŽΞ	FR; heavy chain; light chain; HIV infection.
80	Mus sp.
X 2 3	WO200255668-A2.
당	18-JUL-2002.
PF	11-JAN-2002; 2002WO-US00927;
R X	11-JAN-2001; 2001US-0759112.
PA	(IMMP-) IMMPHERON INC.
2 2 2	Muller S, Kohler H;
# # # # # # # # # # # # # # # # # # #	WPI; 2002-590668/63. N-PSDB; AAL48658.
TG	New polynucleotide encoding a complementarity- or framework-deter

New polynucleotide encoding a complementarity- or framework-determining

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Best Local
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                                       The present invention describes the variable heavy and light chain regions (I) of murine monoclonal antibody (mAB) 1F7. AAY91014 to AAY91016 represent specifically claimed amino acid sequences of the variable light chain, and AAY91017 to AAY91019 represent specifically claimed amino acid sequence of the variable heavy chain. The antibodies are used for treatment of HIV (human immunodeficiency virus) infection and AIDS (acquired immunodeficiency syndrome). They are also used for detecting HIV in serum and for stimulating HIV antigen related and committed B cells to produce broadly reactive and neutralising antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to coding sequences of the murine 1F7 anti-idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primate anti-human immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is a region of the 1F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in vaccines against HIV -
Sequence
                                                                                                                                                                                                                    Variable heavy and light chain regions of murine monoclonal antibody 1F7, useful for treating HIV infection and AIDS \,
                                                                                                                                                                                                                                                                                               Muller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1F7 antibody; murine;
AIDS; anti-HIV; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                          Claim 1; Fig 8; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                          30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               US6057421-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1F7 antibody variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY91019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY91019 standard; protein; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page
                                                                                                                                                                                                                                                                                                                              (IMMP-) IMMPHERON INC
                              clonotypic
                                                                                                                                                                                                                                                                    2000-338622/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVSLTAYAMDY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVSLTAYAMDY 11
                                                                                                                                                                                                                                                                                               Kohler H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                              stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; 27pp;
                                                                                                                                                                                                                                                                                                                                                        94US-0351193
                                                                                                                                                                                                                                                                                                                                                                                     97US-0984277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urine; monoclonal antibody; diagnosis; HIV; human immunodeficiency virus; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H3 amino acid sequence SEQ ID NO:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
0.00012;
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Query; Match

100.0%;

Score

55;

DB 21;

Length

39;

TM27 antibody VH chain mutant

V92R

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RESULT 3
AAO18528
ID AAO1
XX AAO1
XX AAO1
XX AAO1
XX AAO1
XX AAO1
XX MOUG
KW GOMEK
KW GOMEK
KW FR;
XX MO20
PN WO20
XX M11-(
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XX M1
RESULT 4
AAY22433
ID AAY2
XX
AC AAY2
AC AAY2
AC Z8-S
XX
DT 28-S
XX
DE TM27
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                                                                                                                                                                                                                                                                                                                                                  S
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to coding sequences of the murine 1F7 anti-idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or puanti-human immunodeficiency virus (HIV) antibodies and can be used treatment of HIV infection. The present sequence is the 1F7 heavy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in vaccines against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementarity determining region; framewor FR; heavy chain; light chain; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine Mab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO18528 standard;
                                                                             28-SEP-1999
                                                                                                                            AAY22433;
                                                                                                                                                                             AAY22433 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 18-19; 27pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2001; 2001US-0759112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-2002; 2002WO-US00927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200255668-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO18528;
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                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                  1 RVSLTAYAMDY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL48652.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVSLTAYAMDY 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVSLTAYAMDY
                                                                                                                                                                                                                                                                                                      RVSLTAYAMDY 110
                                                                                                                                                                                                                                                                                                                                                                                                 milarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kohler H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB
Pred. No. 0.0
); Mismatches
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mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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                                                                                                                                                                    AAY22429
                                                                                                                                                                                    RESULT 5
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                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
heavy chain.
            IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy;
autoimmune disease; multiple sclerosis; antibody storage; VH;
                                                           TM27 antibody VH chain.
                                                                                           28-SEP-1999
                                                                                                                                                   AAY22429 standard; protein; 120
                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 25-26; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-458611/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-1998;
22-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isotonic pharmaceutical antibody formulations comprising a citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09937329-A1
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                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              have improved
                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
                                                                                                                                                                                                                              RVTATLYAMDY 109
                                                                                                                                                                                                                                                           RVSLTAYAMDY 11
                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                           Conservative
                                                                                       (first entry)
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98SE-0000170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= V92R
                                                                                                                                                                                                                                                                                                         76.4%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              storage
                                                                                                                                                                                                                                                                                           1:
                                                                                                                                                                                                                                                                                                       Score 42;
Pred. No.
                                                                                                                                                    ጅ
                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                         0.8;
                                                                                                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                                                                                                           <u>ب</u>
                                                                                                                                                                                                                                                                                                                       Length 120;
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                           Gaps
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RESULT 6
AAY22430
ID AAY2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC This sequence represents the variable heavy (VH) chain of the cantibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in CC the isotonic pharmaceutical formulation of the invention, along with a CC citrate buffer at a physiologically acceptable pH. The formulations are CC useful in medical therapy, especially for treatment of autoimmune CC disease, and particularly, therapy of multiple sclerosis (using the TM27 CC antibody heavy or light chains). The formulation is useful for improving CC effective. The formulations are stable and have improved storage CC properties. The formulations is simpler than prior art formulations. CC Existing antibody formulations require the use both of a stabiliser and a CC buffer. The present invention formulations are stable only by citrate CC injection. The solution at a physiologically preferable pH. The CC avoidance of low pH prevents undesirable reaction as the site of CC injection. The formulation does not use ovalbumin for stabilisation, CC hence avoiding an allergic response to ovalbumin for stabilisation, CC does not require lyophilisation which is an expensive process and also CC requires the formulation to be resuspended prior to administration.
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Best Local S
Matches 8
                                                                                                                            IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy;
autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;
                                                                                                                                                                                                         28-SEP-1999
                                                                                                                                                                                                                                         AAY22430;
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                               Misc-difference
                                                                             Homo sapiens
                                                                                                                                                                        TM27 antibody VH chain mutant L48I.
                                                                                                                                                                                                                                                                     AAY22430 standard; protein; 120
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22-JAN-1998;
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98SE-0000170
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                                            Location/Qualifiers
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72.7%;
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22-JAN-1998;
    WO9937329-A1
                                                   Misc-difference
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                                                                                                                                                                                                                                                                                            AAY22431;
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                                                                                   Misc-difference
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98SE-0000170.
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                                                                label= F78V
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72.7%;
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Matches
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autoimmune di
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22-JAN-1998;
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                                                                                                                                                                     disease;
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98SE-0000170
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                                                                                   Location/Qualifiers
                                                         68
                               69
                                                                     label= V67L
                 label= M691
                                           label= T68S
                                                                                                                                                                  variable chain; immunoglobulin G; medical therapy; multiple sclerosis; antibody storage; VH; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                    76.48; · 72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42;
Pred. No.
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                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forension sometic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #9037.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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8d.0
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                                                                                                                                                                                                                                                                                        forensic;
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RESULT 10
ABP43853
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CC and to produce other types of data and products dependent on DNA and camino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC specification, but was obtained in electronic format directly from WIPO at the polyment of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specification of the printed specificati
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Best Local Similarity
Matches 6; Conserv
                                                                                                                             Neuroprotective; immunomodulator; cancer; chromosome 12; cytostatic; anti-inflammatory; gene therapy; nutritional suppl wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammativulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                ABP43853 standard; Protein; 391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                         WO200231111-A2
                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                         FLJ20035
                                                                                                                                                                                                                                                                                                                    26-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                  ABP43853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 KMSLNAYALDF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVSLTAYAMDY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                         clone.
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54.5%;
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                                                                                                                                                                                                   supplement;
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18-APR-2002.

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                                                                                                                                                                                                                                                                                                                                                      JLT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnerary, neuroprotective, immunomodulator, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP43544-ABP43989 represent polypeptides encoded by polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
                                                                                                                                                    cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS; cancer; developmental disorder; renal tubular acidosis; anaemia; asthma; mental retardation; neurological disorder; Alzheimer's disease; epilepsy; Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy;
22-JUN-2001; 2001US-300518P
                           20-JUN-2002; 2002WO-US21179
                                                       03-JAN-2003
                                                                                                            Homo sapiens
                                                                                                                                                                                                           Human; nucleic acid-associated protein; NAAP; arteriosclerosis;
                                                                                                                                                                                                                                         Human nucleic acid-associated protein (NAAP) -
                                                                                                                                                                                                                                                                                                                            AAO16433 standard; Protein; 1712 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID # 756; 357pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2000; 2000US-0687527
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                                                                                                                                         Cronn's
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                314
                                                                                                                                                                                                                                                                                                                                                                                                                          1 RVSLTAYAMDY 11
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Yang Y,
                                                                                                                                         disease;
                                                                                                                                                                                                                                                                                                                                                                                                KMSLNAYALDF 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391
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Wehrman
                                                                                                                                        transgenic animal;
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            undi V, Zhang
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                         animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
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                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao
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Query Match
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29-JUN-2001; 2001US-301892P;
29-JUN-2001; 2001US-301893P;
06-JUL-2001; 2001US-303495P;
06-JUL-2001; 2001US-303442P;
15-MAR-2002; 2002US-364438P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gandhi AR,
Arvizu CS,
Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises the amino acid and coding sequences of human nucleic acid-associated proteins (NAAP). The DNA and protein sequences of the invention are useful for diagnosting, treating or preventing disorders associated with aberrant expression of NAAP, such as: cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation); neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of the invention are useful for creating transgenic animals to model human the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequen
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29-JUN-2001; 2001US-301792P
29-JUN-2001; 2001US-301892P
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23-NOV-1995
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Lee SY, Richardson
                     Region
                                                                     Region
                                                                                                                       Region
                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                       Variable heavy chain sequence of humanised antibody chain
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR77303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR77303 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated
                                                                                                                                                                                                                                                    Humanised antibody; TM27; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1635 KMSLNAYALDF 1645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1712 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention.
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                                             /label= CDR1
50..64
/label= DCR2
98..109
/label=
                                                                                                                          Location/Qualifiers 31..35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide; 120
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54.5%; Pre
                                                                                                                                                                                                                                                                                                                                                          entry)
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CDR3
                                                                                                                                                                                                                                                    cell;
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Pred. No.
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                                                                                                                                                                                                                                                    multiple sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents a human nucleic acid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1712;
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Zebarjadian
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RESULT 13
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Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A mouse monoclonal antibody (mAb), TM23, which recognises human V beta 5.2 and 5.3, was humanised by CDR grafting into NEWM heavy chain and REI light chain frameworks. The cDNAs encoding humanised heavy (IgG1) and light (K) chains in mammamlian cell expression vectors with Neo and DHFR selection markers, respectively, were transfected into a DHFR- Chinese hamster fibroblast (CHO) cell line followed by selection and amplification. The humanised MAb that was secreted was designated "TM27", and maintains specificity for human TCR V beta 5.2 and 5.2. It is used as a therapeutic agent for human multiple sclerosis. TM27 is a mutant with Leu at posn. 48 of heavy
                                                                                                                                                                                                                                                                                                                                   AAY91067 standard; Protein; 424 AA.
                                                                                                                     04-MAY-2000
                                                                                                                                           WO200024775-A1
                                                                                                                                                                      Streptomyces nogalater.
                                                                                                                                                                                                Streptomyces nogalater; nogalamycin biosynthesis; antibiotic; anthracycline biosynthetic pathway; gene cluster; drug screening; antibiotic; antitumour antibiotic; anthracyclinone.
                                                                                                                                                                                                                                                     Streptomyces nogalater nogalamycin biosynthesis ORF snogE protein
                                                                                                                                                                                                                                                                                08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 81; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised antibody specific for select sub-population of {\it T} celuseful for treatment of Crohn's disease and Multiple Sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-224322/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9516038-A2
            Ylihonko K,
                                                                23-OCT-1998;
                                                                                         20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin AY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERC/) MERCER (TCEL-) T CELL
                                     (GALI-) GALILAEUS OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 70. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   RVSLTAYAMD 10
                                                                                                                                                                                                                                                                                                                                                                                                      RVTATLYAMD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
            Torkkell S,
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCI INC.
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                                                                98FI-0002295
                                                                                          99WO-FI00870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%;
            Palmu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
            Hakala J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 120;
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RESULT 14
AAP90540
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Best Local S
Matches 7
                                                                                                  Chimeric anti-human immune virus antibodies - contg. mouse variable regions and human constant regions for diagnosis, treatment and prevention of AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP90540 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA39283 represents the nogalamycin biosynthesis gene cluster isolated from Streptomyces nogalater. AAY91055 to AAY91071 represent ORF protein sequences encoded by the gene cluster. Nogalamycin is an anthracycline antibiotic, so the nogalamycin biosynthetic pathway is also known as the anthracycline biosynthetic pathway. DNA fragments, plasmids and process from the present invention are useful for obtaining novel hybrid antibiotics, such as anthracyclines (antitumour antibiotics) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated and purified DNA fragment for obtaining novel hybrid antibiotics comprises the gene cluster for the anthracycline biosynthetic pathway of the bacterium Streptomyces nogalater
Sequence
                                     The H chain variable region is from an immunoglobulin with anti-HIV neutralising activity. See AAN90491, AAN90493 and AAN90495.
                                                                           Claim 2;
                                                                                                                                                      WPI; 1989-229050/32.
N-PSDB; AAN90491, AAN90493, AAN90495
                                                                                                                                                                                                                                                            30-JAN-1988;
08-JUL-1988;
                                                                                                                                                                                                                                                                                                   30-JAN-1989;
                                                                                                                                                                                                                                                                                                                           09-AUG-1989
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                                                                                                                                                                                                                                                                                                                                                                               Mus muscularis.
                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin; H chain variable region; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
20-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA39283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350696/30.
                                                                                                                                                                                                         Maeda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin H chain variable region.
                                                                                                                                                                                               Takatsuki
                        neutralising activity.
(Updated on 25-MAR-2003
                                                                                                                                                                                                                                  (KAGA ) CHEMO
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                                                                          page 14; 33pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVLLTSFAMD 11
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                                                                                                                                                                                             Eda
K;
 119 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                         Y, Kimachi K,
                                                                                                                                                                                                                                  SERO THERAPEUTIC RES INS
                                                                                                                                                                                                                                                            88JP-0020255
88JP-0171385
                                                                                                                                                                                                                                                                                                   89EP-0101583
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                        to correct PA field.)
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Pred. No.
                                                                                                                                                                                                         Tokiyoshi S,
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91;
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Gaps

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RESULT 15
AAR24555
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Best Local Similarity
Marches 6; Conserve
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Query Match
Best Local Similarity
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                                                                                                 The human antibody derived amino acid sequence belongs to the human antibody subgroup I. The CDRs and a part of the amino acid sequence of the neighbouring framework region N- and/or C-terminal are mouse monoclonal antibody derived sequences. The anti-HIV modified antibody can be used for the prophylaxis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human x mouse
                                      Sequence
                                                                                                                                                                                                    New recombinant modified anti-HIV antibodies - comprise human x mouse modified antibody H and L chains
                                                                                                                                                                                                                                             WPI; 1992-212765/26
                                                                                                                                                                                                                                                                                                                                                                      JP04141095-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR24555 standard; Protein; 119 AA
                                                            Specific examples of the H chain are given in AAR24556-58 and AAR24560-62. A specific example of the L chain is given in AAR24575
                                                                                                                                                                            Claim 3; Page 1; 15pp; Japanese.
                                                                                                                                                                                                                                                                                            02-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                             14-MAY-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 TAYAMDY 11
                                       119 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified anti-HIV antibody Heavy chain.
                                                                                                                                                                                                                                                                                            90JP-0266091
                                                                                                                                                                                                                                                                                                                     90JP-0266091
                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= FR3
/note= "human antibody derived amino acid sequence"
99..108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              note= "human antibody derived amino acid sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                        09..119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                    label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "human antibody derived amino acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                            label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= CDR2
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85.7%;
  61.8%;
85.7%;
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  Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody derived
  DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid sequence"
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             Length 119;
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Matches 6; Conservative 1; Mismatches 0; Indels 0;

Qy 5 TAYAMDY 11

Db 102 SAYAMDY 108

Search completed: September 10, 2003, 17:40:19
Job time: 40.05 secs
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